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Best Local Si
Query Match:
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AUTHORS
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AUTHORS
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Homo sapiens clone 23625 mRNA sequence.
AF052135
AF052135.1 GI:3360444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1462)

Andersson, B., "Wentland, M.A., Ricafrente, J.Y., Liu, W. and Gibbs, R.A. A 'double adaptor' method for improved shotgun library construction Anal. Biochem. 236 (1), 107-113 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (05-MAR-1998) Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza S930, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     College of Medicine, One Baylor Plaza Location/Qualifiers
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Direct Submission
                                                                                                                                                                                                                                                                                                                 LeuGlySerAlaValGluValAsnGluAspIleProProArgArgTyrPheArgSerGly 40
     CCCAAAGCAGAAGAGCTGAAGGCAGAGCTGTTAAAACGATATACCAAAGAATATACAGAA
                           ProLysAlaGluGluLeuLysAlaGluLeuLeuLysArgTyrThrLysGluTyrThrGlu 120
                                                                                                     LysSerAlaVallleProGluLysLysAspThrValLysLysLeuLysGluIleAlaPhe 100
                                                                                                                                                                                                                                             ValGluIleIleArgMetAlaSerIleTyrSerGluGluGlyAsnIleGluHisAlaPhe
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                                                                                                                                                 ATCCTCTATAACAAGTATATCACGCTCTTTATTGAGAAACTACCAAAAACATCGAGATTAC 356
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                                                                           AAATCTGCTGTCATTCCTGAAAAGAAAGACACAGTAAAGAAATTAAAGGAGATTGCATTT
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/clone_lib="1NIB"
/dev_stage="infant"
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/sex="female"
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Protein AMSH and cDNA thereof.

235541

E35541.1 GI:18624562

JP 2000139469-A/1.

Homo sapiens (human)
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Command line parameters:

-MODEL-frame+ p2n.model -DEV=xlh
-Q=/Ggn2_1/USPTO_Spool/US08831452/runat_17082004_151159_23641/app_query.fasta_1.583
-DB=GenEmb1 -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER-US09831452_@CGN_1 1_3731 @runat_17082004_151159_23641 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-PGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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36: em_htg_rod:*
37: em_htg_rod:*
38: em_stg.*
40: em_htgo_mus:*
41: em_htgo_other:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Andersson, B., Wentland, M.A., F. A. 'double adaptor' method for A. 'double
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Direct Submission
Submitted (05-MAR-1998) Molecular and Human
College of Medicine, One Baylor Plaza S930,
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Yu, W., Andersson, B., Worley, K.C., Muzny, D.
Ricafrente, J.Y., Wentland, M.A., Lennon, G.
Large-scale concatenation cDNA sequencing
Genome Res. 7 (4), 353-358 (1997)
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CCCAAAGCAGAAGAGCTGAAGGCAGAGCTGTTAAAACGATATACCAAAGAATATACAGAA
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/mol type="mRNA"
/db xref="taxon:9606"
/clone="I.M.A.G.E. Consortium
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JP 2000139469-A/1.
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Patent: JP 2000139469-A 1 23-MAY-2000;
SCIENCE & TECH AGENCY
OS Homo sapiens (human)
PN JP 2000139469-A/1
PD 23-MAY-2000
PF 12-NOV-1998 JP 1998322674
PR KAZUO SUGAMURA,NOBUYUKI TANAKA
PC C12N15/09,C07K14/52,C07K16/24//C12N1
PC C12N121,
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Eukaryota, Metazoa, Chorda
Mammalia, Eutheria, Primat
1 (bases 1 to 1910)
Sugamura, K. and Tanaka, N.
 CAGTTCCATGCCTTCGAGGAGATGATCCGGAACCAGGAGCTAGAAAAAGAGCGACTGAAA
                  GlnPheHisAlaPheGluGluMetIleArgAsnGlnGluLeuGluLysGluArgLeuLys
                                                                                 GluLeuGluLysGluLysGlnArgValAlaGlnGlnLysGlnGlnGlnLeuGluGlnGlu
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                                   Eukaryofa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1930)

Tanaka,N., Kaneko,K., Asao,H., Kasai,H., Endo,Y., Fujita,T., Takeshita,T. and Sugamura,K.

Possible involvement of a novel STAM-associated molecule 'AMSH' intracellular signal transduction mediated by cytokines

J. Biol. Chem. 274 (27), 19129-19135 (1999)
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Submitted (07-0CT-1996) Microbiology, Tohoku University School
Medicine, 2-1 Seizyo-machi Aobaku, Sendai 980-77, Japan
Location/Qualifiers
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IleValGlnGluPheGlyLysValAspProGlyLeuGlyGlyProLeuValProAspLeu
                                                                                                    GluLeuGluLysGluLysGlnArgValAlaGlnGlnLysGlnGlnGlnLeuGluGlnGlu
                                                                                                                                                                                                        ProLysAlaGluGluLeuLysAlaGluLeuLeuLysArgTyrThrLysGluTyrThrGlu
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EC007682

1933 bp mRNA linear PRI 03-OCT-2003 (CDNA clone MGC:3546 IMAGE:3619837), complete cds.

BC007682

BC007682.1 GI:14043381

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1933)

1 (bases 1 to 1933)

2 (Strausberg, R.D., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Altschul, S.F., Jordan, H., More, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Scheetz, T.E., Drange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

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JOURNAL
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AUTHORS
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Pahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
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Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
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Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLML at: http://image.llnl.gov Series: IRAL Plate: 12 Row: 1 Column: 19 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 17738303.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www.nisc.mih.gov/
Contact: nisc.mgc@nigri.nih.gov/
Akhter, N. Ayele, K. Beckstrom-Sternberg, S.M., Benjamin, B.,
Akhter, N. Ayele, K. Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
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Hansen, N. Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J. C.,
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Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E.D.
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Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Gaithersburg, Maryland;
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Submitted (11-MAY-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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/ POTEIN I d. "AAHO7682."

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/ db xref="GI:14043382"

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261 GlyArgLeuCysProGlnPheLeuGlnLeuAlaSerAlaAsnThrAlaArgGlyValGlu
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                                                                                   AlaLeuSerAsnSerGluSerIleProThrIleAspGlyLeuArgHisValValValPro
                                                                                                                                                                                        CysHisThrThrValArgProAlaLysProProValValAspArgSerLeuLysProGly
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                                                                                                                                                                                                                                                                   GAGAAGCCCTCCTTAGATGTGTTCCCCACCTTAACAGTCTCATCCATACAGCCTTCAGAC
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Matches:
Conservative:
Mismatches:
Indels:
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376

316

Alignment Scores:  pred. No.:  1913.00  Matches:  Score:  1913.00  Matches:  Percent Similarity:  91.98\$  Best Local Similarity:  86.64\$  Query Match:  10  Gaps:  US-09-831-452-1 (1-424) x AY083159 (1-1544)  Outline		REFERENCE 1 (bases 1 to 1544) AUTHORS PAWLAK, A. and Guellaen, G. TITLE Direct Submission JOURNAL Submitted (08-MAR-2002) U99, INSERM, Hopital Henri Mondor, Creteil 94010, France FEATURES 11544 /organism="Rattus norvegicus" /mol_type="manna" /db_xref="taxon:10116" CDS /codon_statt=1	AY083159 AY083159 AY083159 AY083159 AY083159 AY083159 AY083159 AY083159 ACCESSION AY083159 AY	Qy  321 LeuileGlnAspGlnGlnGlyLeuileThrLeuGlyTrpIleHisThrHisProThrGln 340
	Db 771 ĠĊĀTTĀĀĠĊGTCATAĠĀĀĀĀGTTTĊĊĊĀĊĊĀĊĀTŤĠĀĀĠĠĊĊĀĊĀTŢĠŦĠĊĠĊ  Qy 261 GlyArgLeuCysProGlnPheLeuGlnLeuAlaSerAlaAsnThrAlaArgGlyValGlu  Db 831 CGCAATCTGTGGTCAGAATTTCTCCAGCTTGCCAGCCCAACACTGCCAAAGGCATCGAG  Qy 281 ThrCysGlyIleLeuCysGlyLysLeuMetArgAsnGluPheThrIleThrHisValLeu  Db 891 ACCTGTGGAGTCCTCTGGGAAATGATGAATGAATGAATCACACATGTCTC  Qy 301 lleProLysGlyIleLeuCysGlyLysLeuMetArgAsnGluPheThrIleThrHisValLeu  Db 891 ACCTGTGGAGTCCTCTGTGGAAAATGAATGAATGAATCACACATGTTCTC  Qy 301 lleProLysGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyG	Db 591 ÄTTGTTCÄÄGÄĞTTCĞĞÄÄĞĞTÄĞÄCÖTTĞĞCCGTGGĞĞĞCTCTGCTGATCTN  Qy 201 GluLysProSerLeuAspValPheProThrLeuThrValSerSerIleGlnProSerAsj	Qy  141 GluLeuGluIysGluIysGlnArgyAlAlaGlnGlnIysGlnGlnGluGlnGluGlnGlu  Qy  141 GluLeuGluIysGluIysGlnArgyAlAlaGlnGlnIysGlnGlnGlnGluGlnGlu  Db  471 GAACTGGAAAAGAAAAGAAAAGAAAGAAGAAGAAGCAGAAGA	

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JOURNAL
MEDLINE
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REFERENCE
AUTHORS
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Mcore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, B.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Boutfard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Schmerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences
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                                                                                                                                                                                                                    NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeff Green/Paturu Kondaiah, NCI.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1735 bp mRNA linear Rattus norvegicus associated molecule with the SH3 dmRNA (cDNA clone MGC:72308 IMAGE:5597943), complete BC061711
Web site: http://www.nisc.nih.gov/
Contact: nisc mgc@nigri.nih.gov/
Contact: nisc mgc@nigri.nih.gov/
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Blakesley,R.W., Bouffard,G.G., Gupta,J., Haghighi,P.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho.S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (05-NOV-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 19924064
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                                                                                                                                          LeuGlySerAlaValGluValAsnGluAspIleProProArgArgTyrPheArgSerGly 40
                                  ValGluIleIleArgMetAlaSerIleTyrSerGluGluGlyAsnIleGluHisAlaPhe
  GTTGAGATCATCCGCATGGCATCCATTTACTCTGAAGAAGGCAACATTGAACATGCCTTT
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//procein_id="AAH61711.1"
//db_xref="G1:38197540"
//db_xref="G1:38197540"
//db_xref="G1:38197540"
//db_xref="G1:38197540"
//translation="MSDHADVSLPPQDRVRILSQLGSAVELNEDIPPRRYFRSGVEII
//translation="MSDHADVSLPPQDRVRILSQLGSAVELNEDIPPRRYKYRFRSGVEII
//translation="MSDHADVSLPPQDRVRILSQLGSAVELNEDIPPRRYKYRFPK
RMASITSEEGNIEHAFILYNKYITHEIEXLPKHRADYKSAIIPPRK
RMASITSEEGNIEHAFILYNKYITHEIEXEERIKGRVAQOKOKOLOGO
ABELKTELLAKYTKYXEQYKERKKEEBELFRYDDLEKKEKORVAQOKOKOLOGO
OFHAPEKMIQKQELEKERLKIVQEFGKVDPGPCGPLLPDLEKKPCVDVAPSSPFSPTQT
SDCNTTIRPAKPPVVDRSLKEGALSVLENKYPTIEGLERIFFMQDDLGLLTLASANIA
KGIETGGLACKLMRAKEFIIHVLERQLGVETGEFFKLTDYGLGLITTGR
HTHPTQTAFLSSVDLHTHCSYQMMLPESIAIVCSPKFQETGFFKLTDYGLQEISTCRQ
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1. .1735
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/clone_lib="NCI_CGAP_Pr49"
/lab_host="DH10B"
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/db_xref="taxon:10116"
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/mol_type="mRNA"
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product="Amsh_protein"
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ATCCCCAGACAAATGGTGGGCCTGATTATTGCCACACAGAGAATGAAGAAGAATTTTC
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                                ThrAspLeuArg 424
                                                                                                AspProProLeuPheCysSerCysSerHisValThrValValAspArgAlaValThrIle
                                                                                                                                            GACTATGGCCTTCAAGAGATTTCAACCTGCCGGCAGAAAGGCTTTCACCCCCATGGCAGA
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               ACAGACCTTCGA
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L8624563

Japiens (human)

Lucaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS
Sugamura, K. and Tanaka, N.
FITLE
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JOURNAL
SCIENCE & TECH AGENCY
OS Homo sapiens (human)
PN J2000139469-A 2 23-MAY-2000;
SCIENCE & TECH AGENCY
OS Homo sapiens (human)
PN J2000139469-A/2
PD J3-MAY-2000
PF 12-NOV-1998 JP 1998322674
PR KAZUO SUGAMURA, NOBUYUKI "
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                                                                                                                                                                                                                                                                                                                                                                                            ATGTCTGACCATGGGGATGTGAGCCTCCCACCCCAAGACCGGGTGAGGATTCTGTCCCAA
                                                                                                                                                                                                                                                                                                                                                                                                             MetSerAspHisGlyAspValSerLeuProProGluAspArgValArgAlaLeuSerGln
                                                                                                                                                                                                                                                              GTTGAGATCATCCGCATGGCGTCCGTTTACTCGGAAGAAGCAACATTGAACATGCCTTT
                    TyrAsnGluGluLysLysLysGluAlaGluGluLeuAlaArgAsnMetAlaIleGlnGln 140
                                                                               ProLysAlaGluGluLeuLysAlaGluLeuLeuLysArgTyrThrLysGluTyrThrGlu
                                                                                                                              AAATCAGCTATCATTCCTGAGAAGAAGATGCTGTCAAGAAATTAAAGAGCGTCGCTTTC
                                                                                                                                                    LysSerAlaValIleProGluLysLysAspThrValLysLysLeuLysGluIleAlaPhe
                                                                                                                                                                                              ATCCTCTACAACAAGTACATCACGCTGTTTATTGAAAAACTTCCGAAAACACCGAGACTAC
                                                                                                                                                                                                               IleLeuTyrAsnLysTyrIleThrLeuPheIleGluLysLeuProLysHisArgAspTyr
   TATAAAGAGCGAAAGAAAAGGAAGAAGAAGAACTTGCCCGAAATATCGCCATCCAGCAA
                                                                 CCTAAAGCGGAAGAGCTGAAGACAGAGCTCTTGAGAAGATACACCAAAGAATATGAGCAG
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56. 1327.
Location/Qualifiers
1. 1384
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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91.75%
83.49%
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Mus musculus Stam binding protein,
IMAGE:4194332), complete cds.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                          ACAGACCTTCGA 1327
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                                                                                   GI:19263555
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RS Strausberg, R.D., Collins, F.S., Wagner, L., Schemen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bondlo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Kodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Boutfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Schmerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl., Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 61 Row: j Column: 3
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 17941276.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genom
Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (05-MAR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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/db_xref="MGI:191777"
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/lab_host="DH10B"
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RMASVYSEEGNIEHAFILYRKYITIFIEKLPKHRDYKSAIIPEKAVAVKKKSVAFPK
ABELKTELLRAYTKYYKGYKGYKEKKKEBEELARNIAIQOELEKEKGRVAQVKKKKOKDGDG
QFHAFEEMIQRQELEKERLKIVQEFGKVDFGPCGFLLPDLEKFCVDVAPSSFSFTQT
PDCNTGMRPAKFPVVDRSLKFGALSVIENVPTIEGLRHIVVPRAUGSEFLQLASANTA
KGIETGGVLGSKLMRNEFITFTYLTE JERQNGGFDYCHTENEEEIFFMQDDLGLTTLGMI
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                                       2 (bases 1 to 2104)
Ishii.N., Aizawa, K. and Sugamura, K.
Direct Submission
Submitted (06-JAN-1998) Kazuo Sugamura, Tohoku University
Medicine, Department of Microbiology and Immunology; 2-1
Seiryo-machi, Aoba-ku, Sendai, Miyagi 980-8575, Japan
(B-mail:sugamura@mail.cc.tohoku.ac.jp, Tel:81-22-717-8096,
Fax:81-22-717-8097)
                                                                                                                                                                                                          Ishii,N., Owada,Y., Yamada,M., Miura,S., Murata,
Kondo,H. and Sugamura,K.
Loss of neurons in the hippocampus and cerebral
                                                                                                                                                                                                                                                                                                  Mus musculus
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Mammalia; Eutheria; Rodentia;
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                                              IleValGlnGlnPheGlyLysValAspProGlyLeuGlyGlyProLeuValProAspLeu
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                                                                                                                                                                                                                GluLeuGluLysGluLysGlnArgValAlaGlnGlnLysGlnGlnGlnLeuGluGlnGlu
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KGIETCGVLCGKLMRNEFTITHVLIPRQNGGPDYCHTENEEEIFFMQDDLGLLTLGWI
HTHPTOTAFLSSVDLHTMCSYQMMLPESTAIVCSPKFQETGFFKLTDYGLQEISTCRQ
KGFHPHGRDPPLFCDCSHVTVKDRIVTITDLR"
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56. .1330
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MGC.
Strausberg, R. L. Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Altschul, S.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haieh, F.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Rosavant, T.L.,
Stapleton, F.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.-U.,
Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
                                                                                                                                                                                                                                                                                                                                                                                      BC003497
Mus musculus Sta
IMAGE:3153829),
                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
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9), complete cds.
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MGC:6953
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TITLE
JOURNAL
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 17941276.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (20-FBB-2001) National Institutes of Health, Mammalian Submitted (20-FBB-2001) National Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Genomics Office, Nati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R. W., Touchman, J. W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length
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Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Den;
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
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Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www.hgsc.bcm.tmc.edu/cdna/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center code: BCM-HGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequencing Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .2477932
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="synonym: Amsh"
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PDCNTGMRPAKEPVVDRSLKPGALSVIENVPTIEGLRHIVVPRNLGSEFLQLASANTA
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                    /note="Mov34; Region: Mov34/MPN/PAD-1 family. Members this family are found in proteasome regulatory subunit eukaryotic initiation factor 3 (eIF3) subunits and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MSDHGDVSLPPQDRVRILSQLGSAVELNEDIPPRRYYRSGVEII
RMASVYSEEGNIEHAFILYNKYITLFIEKLPKHRDYKSAIIPEKKDAVKKLKSVAFPK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="Mammary tumor. Brcal-/fl; MMTV-Cre model. 10 months old, gross tissue." /clone_lib="NCI_CGAP_Mam3" /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
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/db_xref="LocusID:70527"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="Vector: pCMV-SPORT6"
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ry subunits, s and
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regulators of transcription factors. This family is also known as the MPN domain and PAD-1-like domain. It has been shown that this domain occurs in prokaryotes" /db\_xref="CDD:pfam01398"

γQ	Db	Ş	Db Qy	DЬ	ν	Db	γQ	B 4	} {	\$ 5	ф	Ş	Вb	Ş	망	γŞ	ф	Ş	Db	Ş	ДĎ	γQ	В	Ş	B 8	US-09	Align Pred. Score Perce Best 1 Query DB:
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ThrCysGl	CGTAATCT	GlyArgLe	ALALEUSE	TAAC	B	8=	luLysPr	ATTGTTCAA	וייר כל	GlnPheHi	AGTTGG	- <u>5</u>		rAsnG]	CCTAAAGC	roLysA 	CAGO	SerAl	ATCCTCTA	leLeuTy	GTTGAGAT	alGluIl	CTTGGGAG	lyse	MetSerAs	-1 (1-424	res: arity: milarity:
yIleLeuCysGlyI	TCAGAATTI	ysProGlnPhe	rasnserGluseri         ::::   CGTCATAGAAAATG	ÁGGCATGÁGGCCÁ	一片	TTGTGTAGATGTGG	oVal	GAGTTCGGGAAG	מווים!	isAlaPheGluGluMet	AAAAGAAAA	uLysGluLy:	JAAAGAAAAAG	LYSLYS 	GGAAGAGCTGAAG!	aGluGluLeuLys!	TATCATTCCTGAGAAC	aValIle	CAACAAGTACAT	rAsnLysTyrIl	CATCCGCATGGCGT	IleArgMetAla	IGCAGTTGAGT	rAlaValGluV	pHisGlyAspValSer              CCATGGGGATGTGAGC	) x BC003497 (	4.26e-146 1904.00 91.75% 83.49% 86.23%
LysLeuMetArgAsnGl	ä-	uGlnLeuAlaSer	TECCCACCATTGAAC	craagecacergree	laLysProProValVa	CCCCAGCTCACCGT	heProThrLeuThrV		androci	:IleArgAs	CTCAGCAGA	sGlnArgValAlaGlnGlnLy 	AAGAGGAACTTO	GluGluLeu!	JAGCTCTTGAG	/sAlaGluLeuLeuLysAr	BAAAGATGCCGTCAA	SLysAspThrValLy	CACGCTGTTTATTGAAAAA	hrLeuPheIleGluLy	CCGTTTACTCGGAAGA	erIleTyrSerGluGl	CAC.	-6	LeuProPro	2122)	Length: Matches: Conservative: Mismatches: Indels: Gaps:
uPheThrIleThrHisValL	CAATACCGCCAAAGGCATT	aAsnThrAlaArgGlyVal	#TYLEUATGHTSVATVATVATVATVATVATVATVATVATVATVATVATVATV	SGÁCAGGTCCCTGAÁACCT	lAspArgSerLeuLysProGl	CCCACGCAGACTCCAG	erSerIleGlnProSerA	CTGCGGGCTCTGCTCCCTGATCT		nGlnGluLeuGluLysGluArgLeuL	GCAGAAGCAGCTAG	ysGlnGlnGlnLeuGluGlnGlu       :::	AATATCGCCATCC	\laArgAsnMetAlaIleGlnGln 	CAAAGAATATGAGC	sArgTyrThrLysGluTyrThrG .	BAAATTAAAGA	kysLeuLysGluIle	ACTTCCGAAACACCGAGACTA	euProLysHisArgAsp	AGGCAACATTGAACATGCCT	uGlyAsnIleGluHisAlaP	GGCTC	gTyrPheAr	GluaspargValargAlaLeuSerG :::           caagaccgggrgaggarTcTGTCCC		21122 354 35 0
eu 300	AA 891	.Glu 280		À 77	¥	AC 711	sp 220	ი— I	000	00	AG 531	lu 160	AA 471	ln 140	AG 411	1u 120	TC 351	he 100	AC 291	Yr 80	TT 231	he 60	GT 171	17 40	ln 20     AA 111		

Chu-Xia Deng

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JOURNAL
MEDLINE
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AUTHORS
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                                                                                                                                                                                                                                     RS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S. W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Glbbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.,

Generation and initial analysis of more than 15,000 full-length

human and mouse CDNA sequences
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Submitted (27-APR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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                                                                                      Direct Submission
                                                                                                                 Strausberg, R
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mRNA
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                                   US-09-831-452-1 (1-424) x BC006939
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Der
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This clone was selected for full length sequencing because passed the following selection criteria: Hexamer frequency analysis, Similarity but not identity to protein.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clone distribution: MGC clone distribution information can be fo through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 5 Row: h_Column: 19
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Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged,
Gwis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing Center
Center code: BCM-HGSC
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                                                                                                                                                                                                                                                                                                                                        /note="Mov34; Region: Mov34/MPN/PAD-1 family. Members of this family are found in proteasome regulatory subunits, eukaryotic initiation factor 3 (eIF3) subunits and regulators of transcription factors. This family is also known as the MPN domain and PAD-1-like domain. It has bee shown that this domain occurs in prokaryotes" /db_xref="CDD:pfam01398"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MSDHGDVSLPPQDRVRILSQLGSAVELNEDIPPRRYYRGGVEII
RMASVYSEEGNIEHAFILYNKYITLFIEKTPKIRDYKSAIIPEKCOAVXXKSVAFPK
ABELKTELLARYTKYYEQYKERKKKEEELARUAIQCELEKEKQRVAQXKKSVAFQE
QPHAFEEMIQRQELEKERLKIVQEFGKVDPGPCGPLLPDLEKFCVDVAPSSPFSPTQT
PDCNYGMRPAKPPVVDRSLKFGALSVIENVPTIEGLRHIVVPRULCSBFLQLASANTA
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HTHPTQTAFLSSVDLHTHCSYQMMLPESIAIVCSPKFQETGFFKLTDYGLQEISTCRQ
KGFHPHGRDPPLFCDCSHVTVKDRIVTITDLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="Mammary tumor. Brcal-/fl; MMTV-Cre model. months old, gross tissue." /clone lib="NCI CGAP_Mam3" /lab_host="DH10B"
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/db_xref="GI:13905280"
/db_xref="LocusID:70527"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="synonym: Amsh"
/db_xref="LocusID:70527"
/db_xref="MGI:191777"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/strain="129,C57BL/6J,FVB/N"
/db_xref="taxon:10090"
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91.75%
83.49%
86.23%
                                      (1-2172)
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Indels:
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2172 354 35 35 35 0

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	361 GluSerValAlaIleValCysSerProLysPheGlnGluThrGlyPhePheLysLeuThr 380
	341 ThralapheLeuSerSerValaspLeuHisThrHisCysSerTyrGlnMetMetLeuPro 360 
	321 LeuileGlnAspGlnGlnGlyLeuileThrLeuGlyTrpileHisThrHisProThrGln 340 
COmmission	301 IleProLysGlnSerAlaGlySerAspTyrCysAsnThrGluAsnGluGluGluLeuPhe 320
COMMEN	281 ThrCysGlyIleLeuCysGlyLysLeuMetArgAsnGluPheThrIleThrHisValLeu 300 
ANTH TITL JOURN	261 GlyargLeuCysProGlnPheLeuGlnLeuAlaSerAlaAsnThrAlaArgGlyValGlu 280
d	241 AlaLeuSerAsnSerGluSerIleProThrIleAspGlyLeuArgHisValValValPro 260
TITL	221 CysHisThrThrValArgProAlaLysProProValValAspArgSerLeuLysProGly 240
	201 GluLysProSerLeuAspValPheProThrLeuThrValSerSerIleGlnProSerAsp 220
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AUTH	141 GluLeuGluLysGluLysGlrAxgValAlaGlnGlnLysGlnGlnGlnLeuGluGlnGlu 160 
	121 TyrasnGluGluLysLysLysGluAlaGluGluLeuAlaArgAsnMetAlaIleGlnGln 140 
VERSIO KEYWOR SOURCE	101 ProLysalaGluGluLeuLysalaGluLeuLeuLysargTyrThrLysGluTyrThrrGlu 120 
ECOSSS DEFINI	81 LysSerAlaValIleProGluLysLysAspThrValLysLysLeuLysGluIleAlaPhe 100
Db CTTT	61 IleleuTyrAsnLysTyrIleThrLeuPheIleGluLysLeuProLysHisArgAspTyr 80 
אס קל	41 ValGluileIleArgMetAlaSerIleTyrSerGluGluGlyAsnIleGluHisAlaPhe 60 
מם מ	21 LeuGlySerAlaValGiuValAsnGluAspIleProProArgArgTyrPheArgSerGly 40
, p	1 MetSerAspHisGlyAspValSerLeuProProGluAspArgValArgAlaLeuSerGln 20 

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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

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CE 1 (bases 1 to 2455)

RS Strausberg, R. L., Feingold, E. A., Grouse, L. H., Derge, J. G., Klausner, R. D., Collins, F. S., Wagner, L., Shenmen, C. M., Schuler, G. D., Allschul, S. F., Zeeberg, B., Buetow, K. H., Schaefer, C. F., Bhat, N. K., Hopkins, R. F., Jordan, H., Moore, T., Max, S. I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A. A., Rubin, G. M., Hong, L., Scheetz, T. E., Brownstein, M. J., Usdin, T. B., Toshiyuki, S., Scheetz, T. E., Brownstein, M. J., Usdin, T. B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S. S., Loquellano, N. A., Peters, G. J., Abramson, R. D., Mullahy, S. J., Bosak, S. A., McEwan, P. J., McKernan, K. J., Malek, J. A., Gunarathe, P. H., Richards, S., Worley, K. C., Hale, S., Garcia, A. M., Gay, L. J., Hulyk, S. W., Villalon, D. K., Muzny, D. M., Sodergren, E. J., Lu, X., Gibbs, R. A., Fahey, J., Helton, B., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A. C., Shevchenko, Y., Bouffard, G. G., Blakesley, R. W., Touchman, J. W., Green, E. D., Dickson, M. C., Rodriguez, A. C., Grimwood, J., Schmutz, J., Myers, R. M., Butterfield, Y. S., Krzyninski, M. I., Skalska, U., Smallus, D. E., Schnerch, A., Schein, J. E., Jones, S. J. and Marra, M. A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U. S. A. 99 (26), 16899-16903 (2002)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Sumio Sugano
cDNA Library Preparation: Dr. Sumio Sugano
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
cDNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 943
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
contact: (Dickson, Mark) mcd@paxil.stanford.edu
                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (01-AUG-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                              Institute, 31 Center DI
USA
NIH-MGC Project URL: ht
Contact: MGC help desk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATGTCTGAACACACGGACTGCAGTGTGTCGTCAGAGGATCGGGTTCGGGCTCTTACTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MetSerAspHisGlyAspValSerLeuProProGluAspArgValArgAlaLeuSerGln
GluLeuGluLysGluLysGlnArgValAlaGlnGlnLysGlnGlnGlnLeuGluGlnGlu
                                                                                                                                        ProLysAlaGluGluLeuLysAlaGluLeuLeuLysArgTyrThrLysGluTyrThrGlu
                                                                                                                                                                             AAAACCGCCAACATTCCTGAGAAGAAAGAAACGATGAGGAAATTAAAAGGAAATCGCCTTC
                                                                                                                                                                                                                                                  ATCCTGTACAACAATACATCACGTTGTTTATTGAAAAACTTCCCAAACATCGGGAATAC
                                                                                                                                                                                                                                                                        IleLeuTyrAsnLysTyrIleThrLeuPheIleGluLysLeuProLysHisArgAspTyr
                                     TATCTGGTGCGAAAGAGAGCGGAGGATGCGGCTCGGGCTGTGGAAATGTTGAAGCAGCAG
                                                                    TyrAsnGluGluLysLysGluAlaGluGluLeuAlaArgAsnMetAlaIleGlnGln
                                                                                                        CCGAAAGCCGAAGAGCTGAAAAAGTTGCTTCTCAAGCAGTATGACAAAGAGCACGCTGAA
                                                                                                                                                                                                           LysSerAlaValIleProGluLysLysAspThrValLysLysLeuLysGluIleAlaPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IRAK Plate: 122 Row:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Mov34; Region: Mov34/MPN/PAD-1 family. Members of this family are found in proteasome regulatory subunits, eukaryotic initiation factor 3 (eIF3) subunits and regulators of transcription factors. This family is also known as the MPN domain and PAD-1-like domain. It has been shown that this domain occurs in prokaryotes"
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TAFLSSVDLHTHCSYQMMLPESIALVCSPKFNETGYFRLTDYGMDDVGTCKQRGFHPH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_wref="taxon:7955"
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/clone_lib="Sugano SJD adult male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Danio rerio"
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1409.00
77.88%
63.76%
63.81%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (1-2455)
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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 Danio rerio (zebrafish)
Danio rerio
Banio rerio
Bukaryota; Metazoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostei;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 2457)
                                                                                                                                           AY398309 2457 bp mRNA linear VRT 20-OCT-2003 Danio rerio clone RK068A2H11 associated molecule with the SH3 domain of STAM (AMSH) mRNA, complete cds.

AY398309 AY398309
                                                                                                                              AY398309.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LeuIleProLysGlnSerAlaGlySerAspTyrCysAsnThrGluAsnGluGluGluLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LysAspProProLeuPheCysSerCysSerHisValThrValValAspArgAlaValThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GlnThrAlaPheLeuSerSerValAspLeuHisThrHisCysSerTyrGlnMetMetLeu 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GluThrCysGlyIleLeuCysGlyLysLeuMetArgAsnGluPheThrIleThrHisVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GlyAlaLeuSerAsnSerGluSerIleProThrIleAspGlyLeuArgHisValValVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTACACGGACCC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LeuGluLysProSerLeuAspValPheProThrLeuThrValSerSerIleGlnProSer 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IleValGlnGluPheGly---LysValAspProGlyLeuGlyGlyProLeuValProAsp 199
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                                                                                                                                                                                                                                                                      ATGCTGGÁCCTGCGG 1372
                                                                                                                                                                                                                                                                                                      IleThraspLeuarg 424
                                                                                                                                                                                                                                                                                                                                         AAGGACCCGCCCCTCTTCGCTGCTAGTCATCACGTCAGCATCACAGACGGCAGCGTGACC
                                                                                                                                                                                                                                                                                                                                                                                                              ACTGATTATGGGATGGACGATGTCGGTACCTGCAAACAGAGAGGATTCCAACCCTCATCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                 ThrAspHisGlyLeuGluGluIleSerSerCysArgGlnLysGlyPheHisProHisSer 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCAGAGTCCATAGCCATCGTCTGCTCGCCCAAATTCAATGAGACGGGCTACTTCCGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProGluSerValAlaIleValCysSerProLysPheGlnGluThrGlyPhePheLysLeu 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAGACGGCCTTTCTGTCCAGTGTGGATCTGCACACACACTGCTCCTATCAGATGATGCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAGTTCAGCGCCTTCGAGGAGATGATCCGCCGCCAGGAGCTGGAGAAAGAGCGCCGCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PheLeuIleGlnAspGlnGlnGlyLeuIleThrLeuGlyTrpIleHisThrHisProThr
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                                                                                                                              GI:37681728
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                                        Vertebrata; Euteleostomi;
Ostariophysi;
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1357 419 1237

937 279

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259 817

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TITLE
JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Submitted (24-SEP-2003) State Key Lab for Medical Genomics,
Submitted (1997) State Key Lab for Medical Genomics,
Shanghai Institute of Hematology, Ruijin Hospital Affiliated to
Shanghai Second Medical University, 197 Rui Jin Road II, Shanghai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhang, G.W., Sun, X.J., Wu, X.Y., Song, H.D., Zhou, Y., Liu, T.X Deng, M., Sheng, Y., Chen, Y., Ruan, Z., Jiang, C.L., Fan, H.Y., Zon, L.T., Kanki, J.P., Look, A.T. and Chen, Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Song,H.D., Wu,X.Y., Sun,X.J., Zhou,Y., Liu,T.X., Deng,M., Zhang,G.W., Sheng,Y., Chen,Y., Ruan,Z., Jiang,C.L., Fan,H.Y., Zon,L.I., Kanki,J.P., Look,A.T. and Chen,Z. Gene Expression Profiling in the Zebrafish Kidney Marrow Tiss
                                                                                                                                                                                                                          ValGluIleIleArgMetAlaSerIleTyrSerGluGluGlyAsnIleGluHisAlaPhe
                                                                                                                                                                                                                                                                                      LeuGlySerAlaValGluValAsnGluAspIleProProArgArgTyrPheArgSerGly
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                ATGGAGATCATCCGCATGGCCAACATCTACGCCGACGAGGGAAACGTGGAGCACGCCTTC
                                                                                             LysSerAlaValIleProGluLysLysAspThrValLysLysLeuLysGluIleAlaPhe
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                                                                                                                                                                                                                                                                                                                                                    MetSerAspHisGlyAspValSerLeuProProGluAspArgValArgAlaLeuSerGln
                                                                                                                                                                                                                                                                     CTGGGCAGCTCAGTGGACGTGAGCGAGGATGTGCCGCCGCGCAGATACTTCCGCTCCGGC
                                                                              AAAACCGCCAACATTCCTGAGAAGAAAAAACGATGAGGAAATTAAAGGAGATCGCCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 2457)
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PKNPPLFAASHHVSITDGSVTMLDLR"
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1. .2457
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|21. .1377
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62.88%
63.59%
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Matches:
Conservative:
Mismatches:
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Ishii,N., Kuroda,H. and
Direct Submission
Submitted (06-JAN-1998)
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Biochem. Biophys. Res. Commun.
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/mol_type="mRNA"
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                                                                                                                                                       HisThrHisProThrGlnThrAlaPheLeuSerSerValAspLeuHisThrHisCysSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GlnPheHisAlaPheGluGluMetIleArgAsnGlnGluLeuGluLysGluArgLeuLys 180
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 GACATAAAAATAATTGTGTTGGATCTGAGG
                                                                       PheHisProHisSerLysAspProProLeuPheCysSerCysSerHisValThrValVal 414
                                                                                                    GlyPhePheLysLeuThrAspHisGlyLeuGluGluIleSerSerCysArgGlnLysGly 394
                                                                                                                                                                                                                                                              AsnGluGluGluLeuPheLeuIleGlnAspGlnGlnGlyLeuIleThrLeuGlyTrpIle
                                                                                                                                                                                                                                                                                                                                                                                  ThrAlaArgGlyValGluThrCysGlyIleLeuCysGlyLysLeuMetArgAsnGluPhe
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                          AspargalaValThrIleThrAspLeuArg
                                                   TITCATCCACACAAGCAGCCCAGGCTGTTCAGTATATGCAAACATGTGTTGGTAAAA 1311
                                                                                                                                                                       TyrGlnMetMetLeuProGluSerValAlaIleValCysSerProLysPheGlnGluThr
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Search completed: August 23, 2004, 20:50:32
Job time : 5392 secs

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379

CCAAGGACAGATGAATTGAAAAACGACCTTTTAAAGAAATATAACGTAGAATACCAAGAA

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Title:
Perfect score:
Sequence:
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-MODEL-frame+ p2n.model -DEV=xlh
-Q=/Ggn2 1/USPTO_spool/US09831452/runat_17082004_151201_23701/app_query.fasta_1.583
-DB=Pending_Patents_NA_Main -QFMT=fastap -SUFFIX=p2n.rnpm -MINNATCH=0.1
-LOOPEXY=0 -UNITS=bits -START=1 -END=-1 -MARRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pot -THR_MX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFWT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXELN=200000000 -USER=US09831452 @CGN 1 4227 @runat 17082004 151201_23701
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NGSCORES=0 -MAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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2208
                   37577330 seqs, 17593059518 residues
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Listing first 45 summaries
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: /cgn2_6/ptcdata/2/pna/USO96_COMB.seq:*
: /cgn2_6/ptcdata/2/pna/USO7_COMB.seq:*
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29: /cgn2-6/ptodata/2/pna/US096E_COMB.seq; *cgn2-6/ptodata/2/pna/US097B_COMB.seq; *cgn2-6/ptodata/2/pna/US097B_COMB.seq; *cgn2-6/ptodata/2/pna/US097B_COMB.seq; *cgn2-6/ptodata/2/pna/US099B_COMB.seq; *cgn2-6/ptodata/2/pna/US09B_COMB.seq; *cgn2
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/ cgn2_6/ptodata/2/pna/US6045_COMB.seq:*
/ cgn2_6/ptodata/2/pna/US6046_COMB.seq:*
/ cgn2_6/ptodata/2/pna/US6047_COMB.seq:*
/ cgn2_6/ptodata/2/pna/US6049_COMB.seq:*
/ cgn2_6/ptodata/2/pna/US6049_COMB.seq:*
/ cgn2_6/ptodata/2/pna/US6050_COMB.seq:*
/ cgn2_6/ptodata/2/pna/US6050_COMB.seq:*
/ cgn2_6/ptodata/2/pna/US6050_COMB.seq:*
/ cgn2_6/ptodata/2/pna/US6050_COMB.seq:*
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Pred. No. is the score greater than and is derived the the number of results predicted by chance to have a than or equal to the score of the result being printed, i by analysis of the total score distribution.

SUMMARIES

## Result No. 220 218 Score 1000.00 1100.0 Query Match Length DB US-09-488-7258-7586 US-10-170-235-32565 US-10-170-235-32565 US-10-170-235-32565 US-10-170-175-88144 US-10-671-572A-2 US-10-671-572A-2 US-10-752-442-1 US-10-170-235-33766 US-09-682-917-3220 US-09-455-444-3912 US-09-455-444-3912 US-09-682-918-11696 US-09-682-918-11697 US-09-682-918-11698 US-09-682-Sequence 579, App Sequence 32565, A Sequence 32565, A Sequence 2, Appli Sequence 8114, Ap Sequence 8114, Ap Sequence 8114, Ap Sequence 331, Ap Sequence 331, Ap Sequence 1093, A Sequence 1093, A Sequence 11095, Ap Sequence 2597, Ap Sequence 7324, Ap Sequence 7323, Ap Sequence 5172, Ap Sequence 7325, Ap Sequence 7325, Ap Sequence 7325, Ap Sequence 7325, Ap Sequence 2547, Description

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GIVER CONTROL	D:: 1.49e-173 Length: 1591  Similarity: 100.00% Matches: 0 cal Similarity: 100.00% Mismatches: 0 atch: 100.00% Indels: 0 atch: 20 Gaps: 0  31-452-1 (1-424) x US-09-471-275-579 (1-1591)  1 MetSerAspHisGlyAspValSerLeuProProGluAspArgValArgAlaLeuSe	TITLE OF INVENTION: Novel Contigs Obtained TITLE OF INVENTION: Prom Various Libraries FILE REPERENCE: 782 CURRENT PILLING DATE: 1999-12-23 CURRENT FILLING DATE: 1999-01-20 EARLIER APPLICATION NUMBER: US 09/234,611 EARLIER APPLICATION NUMBER: US 09/234,611 EARLIER APPLICATION NUMBER: US 09/240,371 EARLIER APPLICATION NUMBER: US 09/277,227 EARLIER APPLICATION NUMBER: US 09/277,227 EARLIER FILLING DATE: 1999-01-29 EARLIER FILLING DATE: 1999-03-25 EARLIER FILLING DATE: 1999-03-18 EARLIER FILLING DATE: 1999-03-19 EARLIER FILLING DATE: 1999-03-18 EARLIER FILLING DATE: 1999-03-19 EARLIER FILLING DATE: 1999-03-25 EARLIER FILLING DATE: 1999-03-26 EARLIER FILLING DATE: 1999-03-27 EARLIER FILLING DATE: 1999-03-27 EARLIER FILLING DATE: 1999-03-26 EARLIER FILLING DATE: 1999-03-27 EARLIER FILLING DATE: 1999-03-27 EARLIER FILLING DATE: 1999-03-26 EARLIER FILLING DATE: 1999-03-27 EARLIER FILLING DATE: 1999-03-26 EARLIER FILLING DATE: 1999-03-27 EARLIER FILLING DATE: 1999-03-26 EARLIER FILLING DATE: 1999-03-27 EARLIER FILLING DATE: 1999-03-27 EARLIER FILLING DATE: 1999-03-27 EARLIER FILLING DATE: 1999-03-27 EARLIER FILLING DATE: 1999-03-26 EARLIER FILLIN

lease 114,

RESULT 1 US-09-471-275-579 ; Sequence 579, Application US/09471275 ; GENERAL INFORMATION: ; APPLICANT: Hyseq, Inc.

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GlyArgLeuCysProGlnPheLeuGlnLeuAlaSerAlaAsnThrAlaArgGlyValGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GluLeuGluLysGluLysGlnArgValAlaGlnGlnLysGlnGlnGlnLeuGluGlnGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LeuIleGlnAspGlnGlnGlyLeuIleThrLeuGlyTrpIleHisThrHisProThrGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AlaLeuSerAsnSerGluSerIleProThrIleAspGlyLeuArgHisValValValPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CysHisThrThrValArgProAlaLysProProValValAspArgSerLeuLysProGly
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                                                                                                                                                                                                           AspProProLeuPheCysSerCysSerHisValThrValValAspArgAlaValThrIle
                                                                                                                                                                                                                                                                                                       AspHisGlyLeuGluGluIleSerSerCysArgGlnLysGlyPheHisProHisSerLys
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Pred. No.:
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NAME/KEY: misc feature
LOCATION: (199)...(1472)

OTHER INFORMATION: similar to gi4098124 in the genepept database
OTHER INFORMATION: Run with FASTXY 3.3t00, default parameters
US-09-488-725B-7586
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CCURRENT APPLICATION NUMBER: US/09/488,725B
CCURRENT FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/004,182
PRIOR APPLICATION NUMBER: US 09/034,341
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-05-26
PRIOR APPLICATION NUMBER: US 09/131,598
PRIOR APPLICATION NUMBER: US 09/170,294
PRIOR FILING DATE: 1998-08-10
PRIOR FILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: US 09/170,294
PRIOR FILING DATE: 1998-10-27
PRIOR APPLICATION NUMBER: US 09/179,473
PRIOR APPLICATION NUMBER: US 09/179,473
PRIOR APPLICATION NUMBER: US 09/181,430
PRIOR FILING DATE: 1998-10-28
PRIOR APPLICATION NUMBER: US 09/235,076
PRIOR APPLICATION NUMBER: US 09/234,611
PRIOR APPLICATION NUMBER: US 09/234,611
PRIOR FILING DATE: 1999-01-22
PRIOR FILING DATE: 1998-01-28
PRIOR APPLICATION NUMBER: US 09/234,611
PRIOR APPLICATION DATE: 1999-01-29
PRIOR APPLICATION NUMBER: US 09/234,611
PRIOR APPLICATION DATE: 1999-01-29
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NUMBER OF SEQ ID NOS: 10289
SOFTWARE: pt CT genes Version 1.01
SEQ ID NO 7586
LENGTH: 1591
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APPLICANT: Chenghua Liu
APPLICANT: Radoje T. Drmanac
TITLE OF INVENTION: Novel Cont
TITLE OF INVENTION: From Var:
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APPLICANT: John Tillinghast
APPLICANT: Ankura Sinku
APPLICANT: Chenghua Liu
APPLICANT: Radoje T. Drmana
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RESULT 2
US-09-488-725B-7586
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US-10-170-235-32565
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TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN
TITLE OF INVENTION: TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF
FILE REFERENCE: CLOOL380
CURRENT APPLICATION NUMBER: US/10/170,235
CURRENT FILING DATE: 2003-03-17
NUMBER OF SEQ ID NOS: 42514
SEQ ID NO 32565
LENGTH: 1767
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ilar Simi ::	FEATURE: ; NAME/KEY: CDS ; LOCATION: 111282 US-09-831-452-2 Alignment Scores:	NUMBER OF SEQ ID NOS: 4  SOFTWARE: PatentIn Ver. 2.0  SEQ ID NO 2  LENGTH: 1910  TYPE: DNA ORGANISM: Homo ganiens	; CURRENT APPLICATION NUMBER: US/09/831,452 ; CURRENT FILING DATE: 2001-07-10 ; PRIOR APPLICATION NUMBER: PCT/JP99/06309 ; PRIOR FILING DATE: 1999-11-12 ; PRIOR APPLICATION NUMBER: JO . 10-322674 : PRIOR APPLICATION NUMBER: JP . 10-322674	; Sequence 2, Application US/09831452 ; GENERAL INFORMATION: ; APPLICANT: SUGAMURA, Kazuo ; APPLICANT: TANAKA, Nobuyuki ; TITLE OF INVENTION: Protein AMSH and cDNA thereof ; FILE REFERENCE: 2001-0572A/LC/00653	49 AC	TTCTGTAGCTGCAGCCACGTGACTGTTGTGG		rVallalleVallysserProL             AGTAGCCATIGTTTGCTCCCCA	341 ThrAlaPheLeuSerSerValAspLeuHisThrHisCysSerTyrGlnMetMetLeuPro 3	Qy 321 LeuileGlnAspGlnGlnGlyLeuileThrLeuGlyTrpIleHisThrHisProThrGln 340 	Qy 301 IleProLysGlnSerAlaGlySerAspTyrCysAsnThrGluAsnGluGluIeuPhe 320	Qy 281 ThrCysGlyIleLeuCysGlyLysLeuMetArgAsmGluPheThrIleThrHisValLeu 300	Db 909 GCACTGAGCAACTCAGAAAGTATTCCCACAATCGATGGATG
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321 LeulleGlnAspGlnGlnGlyLeulleThrLeuGlyTrpIleHisThrHisPxoThrGln 340 [	851 ACATGREGAATTCTCTGTGGAAAACTGATGAGGAATGAATTTACCCATGACCCATGTTCTC 910 301 IleProLysGlnSerAlaGlySerAspTyrCysAsnThrGluAsnGluGluGluGubeuPhe 320	261 GlyArgLeuCysProGlnPheLeuGlnLeuAlaSerAlaAsnThrAlaArgGlyValGlu 280	671 TGTCACACAACTGTAAGGCCAGCTAAGCCACCTGTGGTGGACAGGTCCTTGAAACCTGGA 730 241 AlaLeuSerAsnSerGluSerIleProThrIleAspGlyLeuArgHisValValValPro 260	01 GlulysproSerLeulapValPheProThrLeuThrValSerSerIleGInProSerAsp	IleValGlnGluPheGlyLysValAspProGlyLeuGlyGlyProLeuValProAspLeu 2	161 GlnPheHisAlaPheGluGluMetIleArgAsnGlnGluLeuGluLysGluArgLeuLys 180 	41 GluLeuGluLysGluLysGlnArgValAlaGlnGlnLysGlnGlnGlnLeuGluGlnGlu 	311 CCCAAAGCAGAAGACTGAAGGCAGAGCTGTTAAAACGATATACCAAAGAATATACAGAA 370 121 TyrasnGluGluLysLysLysGluAlaGluGluLeuAlaArgAsnMetAlaIleGlnGln 140	51 AAATCTGCTGTCATTCCTGAAAAAGAAGACACAGTAAAGAAATTAAAGGAGATTGCATTT 01 ProlysalaGluGluLeuLysalaGluLeuLeuLysargTyrThrLysGluTyrThrGlu		131 GTIGHAGATTATCCGAATGGCATCCATTTACTCTGAGGAAGGAAG		AspHi

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; TYPE: DNA; CORGANISM: Homo sapider FEATURE: FEATURE: CDS; LOCATION: 11.1282
US-10-671-572A-2
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GENERAL INFORMATION:
APPLICANT: SUGAMURA, Kazuo
APPLICANT: TANAKA, Nobuyuki
TITIE OF INVENTION: Protein AMSH and CDNA thereof
FILE REFERENCE: 2003-1382/WMC/00653
CURRENT APPLICATION NUMBER: US/10/671,572A
CURRENT FILING DATE: 2003-09-29
PRIOR APPLICATION NUMBER: 09/81,452
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: PCT/JP99/06309
PRIOR APPLICATION NUMBER: JP No. 10-322674
PRIOR FILING DATE: 1999-11-12
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SOFTWARE: PatentIn Ver. 2.0
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RESULT 6
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; GENERAL INFORMATI:
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Sequence 8814, Application US/09770175
GENERAL INFORMATION:
APPLICANT: Gearing, David P.
APPLICANT: Holtzman, Douglas A.
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; TYPE: DNA
; ORGANISM: Homo sapiens
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Sequence 1, Application US/10752442

Sequence 1, Application US/10752442

APPLICANT: Itch, Sumiko

APPLICANT: Itch, Susumu

APPLICANT: Heldin, Carl-Henrik

APPLICANT: Heldin, Carl-Henrik

APPLICANT: Heldin, Carl-Henrik

APPLICANT: Western US/10/752,442

FILE REFERENCE: L0461.70096US01

CURRENT APPLICATION NUMBER: US/10/752,442

CURRENT FILING DATE: 2004-01-06

PRIOR APPLICATION NUMBER: US 09/665,479

PRIOR APPLICATION NUMBER: US 60/154,846

PRIOR FILING DATE: 1909-09-20

PRIOR FILING DATE: 1999-09-20

NUMBER OF SEQ ID NOS: 20

SOFTWARE: Patentin version 3.2

SEQ ID NO 1

LENGTH: 2003
Percent Similarity:
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Query Match:
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Sequence 331, Application US/09881797

Sequence 331, Application US/09881797

; GENERAL INFORMATION:

APPLICANT: Tim Keith

TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES

TITLE OF INVENTION: RELATING TO RESPIRATORY DISEASES AND OBE;

FILE REFERENCE: HUM01-04

; CURRENT APPLICATION NUMBER: US/09/881,797

; CURRENT FILING DATE: 2001-06-14

pRIOR APPLICATION NUMBER: 60/211,749

pRIOR PILING DATE: 2000-06-14

volumer of Seq ID NOS: 4687

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 3931

; LENGTH: 2045

; TYPE: DNA

; ORGANISM: Human

US-09-881-797-3931
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Best Local Similarity
Query Match:
DB:
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US-09-881-797-3931/c
US-09-881-797-3931, Application US/09881797
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                   ProLysAlaGluGluLeuLysAlaGluLeuLeuLysArgTyrThrLysGluTyrThrGlu 120
                                                             AAATCTGCTGTCATTCCTGAAAAGAAAGAACACAGTAAAGAAATTAAAGGAGATTGCATTT
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Matches:
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RESULT 9
US-10-021-698-3931/c
Sequence 3931, Application US/10021698
GENERAL INFORMATION:
APPLICANT: Tim Keith
TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID
TITLE OF INVENTION: RELATING TO RESPIRATORY D
FILE REFERENCE: HUM01-04
FILE REFERENCE: HUM01-04
 CURRENT APPLICATION
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NUMBER: US/10/021,
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; ORGANISM: Human
US-10-021-698-3931
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PRIOR APPLICATION NUMBER: 60/211,74
PRIOR FILING DATE: 2000-06-14
NUMBER OF SEQ ID NOS: 4687
SOFTWARE: FASTSEQ for Windows Versi
SEQ ID NO 3931
LENGTH: 2045
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Sequence 4025, Application US/60213362

GENERAL INFORMATION:
APPLICANT: Morris, MacDonald
APPLICANT: Lal, preeti
APPLICANT: Lal, preeti
APPLICANT: Disp, Dinh
TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
TITLE OF INVENTION: Polymuclectide Sequence Databases, and Single Nuclectide Polymor
FILE REFERENCE: GX-0016 p
CURRENT APPLICATION NUMBER: US/60/213,362
CURRENT APPLICATION NUMBER: US/60/213,362
CURRENT FILING DATE: 2000-06-21
NUMBER OF SEQ ID NOS: 8429
SOFTWARE: PERL Program
LENGTH: 2087
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: 235222.9
US-60-213-362-4025
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Pred. No.:
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Percent Similarity:
Best Local Similarity:
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                                                                           ThrAlaPheLeuSerSerValAspLeuHisThrHisCysSerTyrGlnMetMetLeuPro
                                                                                                              CTCATACAGGATCAGCACGGCCTCATCACACTGGGCTGGATTCATACTCACCCCACACAC
                                                                                                                           LeuIleGlnAspGlnGlnGlyLeuIleThrLeuGlyTrpIleHisThrHisFroThrGln
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                                                             ACCGCGTTTCTCCAGTGTCGACCTACACACTCACTGCTCTTACCAGATGATGTTGCCA
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; NAME/KEY: misc_feature; OTHER INFORMATION: Inc; US-60-278-561-6951
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US-60-278-561-6951
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GENERAL INFORMATION:
APPLICANT: Morris, MacDonald
APPLICANT: Lal, Preeti
APPLICANT: Diep, Dinh
TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
TITLE OF INVENTION: Polymucleotide Sequence Databases, and Single Nucleotide
TITLE OF INVENTION: Polymorphisms Identified Thereby
FILE REFERENCE: GX-0012-1 p
CURRENT APPLICATION UNMERR: US/60/278,561
CURRENT APPLICATION TO BE SEQUENCE OF THE PROBLEM OF O
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Sequence 16983, Application US/60324185

Sequence 16983, Application US/60324185

Sequence 16983, Application US/60324185

Sequence 16983, Applicantion, MacDonald

APPLICANT: Mar. Preeti

APPLICANT: Diep, Dinh

TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING

TITLE OF INVENTION: POLYMORPHISMS IDENTIFIED THEREBY

FILE REFERENCE: GX-0019-1 P

FILE REFERENCE: GX-0019-1 P

FILE REFERENCE: GX-0019-1 P
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NUMBER OF SEQ ID NOS: 35862
SOFTWARE: PERL Program
SEQ ID NO 16983
LENGTH: 2087
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OTHER INFORMATION:
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ORGANISM: Homo sapiens
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 AlaLeuSerAsnSerGluSerIleProThrIleAspGlyLeuArgHisValValValPro
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SEQUENCE STATES APPLICANT: VENTER, J. Craig
APPLICANT: VENTER, J. Craig
TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN
TITLE OF INVENTION: TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF
FILE REFERENCE: CL001380
CURRENT APPLICATION NUMBER: US/10/170,235
CURRENT APPLICATION ON THE SUCH AS NUMBER OF SEQ ID NOS: 42514
SEQ ID NO 33766
LENGTH: 2091
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GENERAL INFORMATION:
APPLICANT: HOltzman, Douglas A.
APPLICANT: Myers, Paul
APPLICANT: Myers, Paul
APPLICANT: Gearing, David P.
APPLICANT: Pan, Yang
ITITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.1129-001
CURRENT APPLICATION NUMBER: US/09/606,776
CURRENT FILING DATE: 1999-06-27
PRIOR APPLICATION NUMBER: 60/141,578
PRIOR APPLICATION NUMBER: 60/141,379
PRIOR APPLICATION NUMBER: 60/141,379
PRIOR APPLICATION NUMBER: 60/141,379
PRIOR APPLICATION NUMBER: 60/141,379
PRIOR APPLICATION NUMBER: 60/141,38
PRIOR APPLICATION NUMBER: 60/141,38
PRIOR APPLICATION NUMBER: 60/141,138
PRIOR APPLICATION NUMBER: 60/141,581
PRIOR APPLICATION NUMBER: 60/141,581
PRIOR FILING DATE: 1999-06-28
PRIOR APPLICATION NUMBER: 60/141,581
PRIOR FILING DATE: 1999-06-29
SEQ ID NO 4875
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US-09-606-776-4875
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                   TATAATGAAGAAAGAAGGAAGGAAGGAATTGGCCCGGAACATGGCCATCCAGCAA 1040
                                            TyrAsnGluGluLysLysLysGluAlaGluGluLeuAlaArgAsnMetAlaIleGlnGln 140
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Sequence 3220, Application US/09652917
(GENERAL INFORMATION:
APPLICANT: Shyjan, Andrew W.
APPLICANT: Holtzman, Douglas A.
APPLICANT: Distefano, Peter
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLE
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.1170-001
CURRENT APPLICATION NUMBER: US/09/652,917
CURRENT APPLICATION NUMBER: 60/151,422
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US-09-652-917-3220
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NUMBER OF SEQ ID NOS: 3855
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 3220
LENGTH: 2541
TYPE: DNA
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            GlyArgLeuCysProGlnPheLeuGlnLeuAlaSerAlaAsnThrAlaArgGlyValGlu
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Search completed: August 23, 2004, 23:02:22 Job time : 4365 secs

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/cgn2_6/ptodata/2/pna/US08_COMB.seq:*
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49. /cgn2_6/ptodata/2/pna/US101B_COMB_seq:
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56. /cgn2_6/ptodata/2/pna/US101B_COMB_seq:
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68. /cgn2_6/ptodata/2/pna/US1001C_COMB_seq:
69. /cgn2_6/ptodata/2/pna/US1002C_COMB_seq:
69. /cgn2_6/ptodata/2/pna/US1003C_COMB_seq:
69. /cgn2_6/ptodata/2/pna/US1003C_C
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

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RESULT 1

US-09-831-452-2

Sequence 2, Application US/09831452

GENERAL INFORMATION:
APPLICANT: SUGAMURA, Kazuo
APPLICANT: SUGAMURA, Nobuyuki
TITLE OF INVENTION: Protein AMSH and cDNA the
FILE REFERENCE: 2001-0572A/LC/00653
CURRENT PILING DATE: 2001-07-10
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: PCT/JP99/06309
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-11-12
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SECTUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEC ID NO 2
LENGTH: 1910
TYPE: DNA
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CURRENT APPLICATION NUMBER: US/10/671,572A
CURRENT FILING DATE: 2003-09-29
PRIOR APPLICATION NUMBER: 09/831,452
PRIOR APPLICATION NUMBER: 09/831,452
PRIOR APPLICATION NUMBER: 09/831,452
PRIOR FILING DATE: 2001-07-10
PRIOR PILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: DATE: 1999-11-12
PRIOR APPLICATION NUMBER: DATE: 1998-11-12
NUMBER OF SEQ ID NOS: 4
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TITLE OF INVENTION: HOWEL NUCLEIC ACID MOLECULES AND
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1000.2058-001
CURRENT APPLICATION NUMBER: US/09/770,175
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: US 60/178,874
PRIOR APPLICATION NU
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GENERAL INFORMATION:
APPLICANT: Gearing, David P.
APPLICANT: Holtzman, Douglas A.
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Best Local Similarity
Matches 1910; Conserv
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CAATAAGGGCATCTGTGCAGAAATTTGGAAGCCATTTAGAAAATCTTTTTGGATTTTCCTG
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ACATGCCTTCATCCTCTATAACAAGTATATCACGCTCTTTATTGAGAAAACTACCAAAACA

ACATGCCTTCATCCTCTATAACAAGTATATCACGCTCTTTATTGAGAAACTACCAAAACA

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61 TCTCTCCCAGCTGGGTAGTGCGGTAGAGGTGAATGAAGACATTCCACCCCGTCGGTACTT

TCTCTCCCAGCTGGGTAGTGCGGTAGAGGTGAATGAAGACATTCCACCCCGTCGGTACTT

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Sequence 1, Application US/10752442

SEQUENCE 1, MPDICANT: ITCh, Fumiko

APPLICANT: ITCh, Susumu

APPLICANT: ITCh, Susumu

APPLICANT: Heldin, Carl-Henrik

APPLICANT: Heldin, Carl-Henrik

APPLICANT: ten-Dijke, Peter

TITLE OF INVENTION: SMAD ASSOCIATING POLYPEPTIDES

FILE REFERENCE: L0461 70096US01

CURRENT FILING DATE: 2004-01-06

PRIOR APPLICATION NUMBER: US 09/665,479

PRIOR APPLICATION NUMBER: US 09/665,479

PRIOR APPLICATION NUMBER: US 60/154,846

PRIOR APPLICATION NUMBER: US 60/154,846

PRIOR FILING DATE: 1999-09-20

NUMBER OF SEQ ID NOS: 20

SOFTWARE: PatentIn version 3.2

SEQ ID NO 1

LENGTH: 2003
                                                                                                                                                  ; NAME/KEY: CDS
; LOCATION: (63)..(1334)
US-10-752-442-1
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                                                           Query Match 100.0%; Score 1910;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1910; Conservative 0; Mismatches
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ORGANISM: Homo sapiens
FEATURE:
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RESULT 5
US-09-881-797-3931/c
US-09-881-797-3931/c
; Sequence 3931, Application US/09881797
; GENERAL INFORMATION:
APPLICANT: Tim Keith
; TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: RELATING TO RESPIRATORY DISEASES AND CURRENT APPLICATION NUMBER: US/09/881,797
; CURRENT APPLICATION NUMBER: 60/211,749
PRIOR APPLICATION NUMBER: 60/211,749
PRIOR APPLICATION NUMBER: 60/211,749
PRIOR FILING DATE: 2000-06-14
NUMBER OF SEQ ID NOS: 4687
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3931
LENGTH: 2045
                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Human
US-09-881-797-3931
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Qy 121 CCGCTCTGGAGTTGAGATTATCCGAATGGCATCCATTTACTCTGAGGAAGGCAACATTGA 180	1321 CCATATCAGTGTACTGTAGCCCCTTAATTTAAGCTTTCTAGAAAGCTTTGGAAGTTTTTG 1380	95 55
Qy 61 TCTCTCCCAGCTGGGTAGTGCGGTAGAGAGATGAAGACATTCCACCCCGTCGGTACTT 120	1261 AGTGACCATCACAGACCTTCGATGAGCGTTTGAGTCCAACACCTTCCAAGAACAACAACAAA 1320 	A 46
QY 1 CTTGGTCCTGATGTCTGACCATGGAGATGTGAGCCTCCCGCCCG	1201 ACACAGCAAGGATCCACCTCTGTTCTGTAGCTGCAGCCACGTGACTGTTGTGGACAGAGC 1260	å S
Query Match 100.0%; Score 1910; DB 43; Length 2045; Best Local Similarity 100.0%; Pred. No. 0; Matches 1910; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	1141 TAAACTGACCATGGACTAGAGGAGATTTCTTCCTGTCGCCAGAAAGGATTTCATCC 1200 	β δ
; TYPE: DNA ; ORGANISM: Human US-10-021-698-3931	1081 GATGTTGCCAGAGTCAGTAGCCATTGTTTGCTCCCCCAAGTTCCAGGAAACTGGATTCTT 1140	B 8
NUMBER OF SEQ ID NOS: 4687  SOFTWARE: FastSEQ for Windows Version 4.0  SEQ ID NO 3931  FENCEUR: 2046	1021 CCCCACACAGACCGCGTTTCTCTCCAGTGTCGACCTACACACTCACT	B 8
CURRENT APPLICATION NUMBER: US/10/021,698 ; CURRENT FILING DATE: 2001-10-22 ; PRIOR APPLICATION NUMBER011,749 ; PRIOR APPLICATION NUMBER06/211,749	961 AGAACTTITCCTCATACAGGATCAGCAGGGCCTCATCACACTGGGCTGGATTCATACTCA 1020 	라 &
APPLICANT: Tim Keith TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES TITLE OF INVENTION: RELATING TO RESPIRATORY DISEASES AND OBESITY FILE REFERENCE: HIMOI-04	901 CCATGTTCTCATCCCCAAGCAAAGTGCTGGGTCTGATTACTGCAACACAGAGAACGAAGA 960 	β Q
RESULT 6 US-10-021-698-3931/c ; Sequence 3931, Application US/10021698 ; GENERAL INFORMATION:	841 GGGAGTGGAGACATGTGGAATTCTCTGTGGAAAACTGATGAGGAATGAAT	라 장
	781 GGTGGTGCCTGGGCGGCTGTGCCCACAGTTTCTCCAGTTAGCCAGTGCCAACACTGCCCG 840	D Qy
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	301 GATTGCATTTCCCAAAGCAGAAGAGCTGAAGGCAGAGCTGTTAAAACGATATACCAAAGA 360 	Ag Ag

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RESULT 7
US-10-170-235-33766
[Sequence 33766, Application US/10170235]
[SEQUENCE 33766, Application US/10170235]
[SENERAL INFORMATION:
[APPLICANT: VENTER, J. Craig
[APPLICANT: VENTER, J. Craig
[TITLE OF INVENTION: TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF
[TITLE OF INVENTION: TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF
[FILE REFERENCE: CL001380
[CURRENT APPLICATION UNMER: US/10/170,235]
[CURRENT FILING DATE: 2003-03-17
[NUMBER OF SEQ ID NO 33766
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                                                           ACCAGATTGTTTGGCTAACACATCCCGAAGAATGATTTTGTCAGGAATTATTGTTATTTA
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RESULT 8
US-09-606-776-4875
; Sequence 4875, Application US/09606776
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Holtzman, Duglas A.
; APPLICANT: Gearing, David P.
APPLICANT: Pan, Yang
; TITLE OF INVENTION: THEREFOR
; TITLE OF INVENTION: THEREFOR
; TITLE OF INVENTION: THEREFOR
; TITLE OF INVENTION: MUMBER: US/09/606,776
; CURRENT FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/141,578
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: 60/141,379
; PRIOR FILING DATE: 1999-06-28
; PRIOR PRILING DATE: 1999-06-28
; PRIOR PRILING DATE: 1999-06-28
; PRIOR FILING DATE: 1999-06-28
; PRIOR FILING DATE: 1999-06-28
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 5415
; SOFTWARZ: FASESEQ for Windows Version 3.0
; SEQ ID NO 4875
; LENGTH: 2541

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AGAACTITICCTCATACAGGAICAGCAGGGCCTCATCACACTGGGCTGGATTCATACTCA
                                                   CCATGTTCTCATCCCCAAGCAAAGTGCTGGGTCTGATTACTGCAACACAGAGAACGAAGA
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  RESULT 9
US-09-652-917-3220
INS-09-652-917-3220
SEQUENCE 3220, Application US/09652917
GENERAL INFORMATION:
APPLICANT: Shyjan, Andrew W.
APPLICANT: Distefano, Douglas A.
APPLICANT: Distefano, Peter
ITILE OF INVENTION: NOVEL NUCLEIC ACID
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CURRENT FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: 60/151,422
PRIOR FILING DATE: 1999-08-30
NUMBER OF SEQ ID NOS: 3855
SOFTWARE: FastSEQ for Windows Version 4.1
SEQ ID NO 3220
LENGTH: 2541
TYPE: NAS41
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US-09-699-998-10797
; Sequence 10797, Application US/0969998
; GENERAL INFORMATION:
APPLICANT: Holtzman, Douglas A.
APPLICANT: Holtzman, Dovid P.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND TITLE OF INVENTION UNMEER: US/09/699,998
; CURRENT APPLICATION NUMBER: US/09/699,998
; CURRENT FLING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: 60/162,362
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 1095
; SOPTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 10797
; LENGTH: 2541
TYPE: DNA
; ORGANISM: Homo sapiens
US-09-699-998-10797
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Qy 421 CATCCAGCAAGAGCTGGAAAAGGAAAACACAAGGGTAGCACAACAGAAGCAGCAAGTT 480	Oy  301 GATTGCATTCCCAAAGCAGAAGAGGCTGAAGGCAGAGCTGTTAAAACGATATACCAAAGA 360	OY  181 ACATGCCTTCATCCTCTATAACAAGTATATCACGCTCTTTATTGAGAAACTACCAAAACA 240	Qy 61 TCTCTCCAGCTGGGTAGTGCGGTAGGTGAATGAAGACATTCACCCCGTCGGTACTT 120	Query Match  100.0%; Score 1910; DB 31; Length 2541;  Best Local Similarity 100.0%; Pred. No. 0;  Matches 1910; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  Qy 1 CTTGGTCCTGATGTCTGACCATGGAGATGTGAGCCTCCCGCCCG	SOFTWARE: FASTSEQ for Windows Version 4.0 SEQ ID NO 2597 ENGTH: 2541 TYPE: DNA CRGANISM: Homo sapiens US-09-726-810-2597	ICE: 1600 ICATION N ING DATE: CATION NUM DATE: 1	APPLICANT: Gearing, David P. APPLICANT: Holtzman, Douglas A. TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES TITLE OF INVENTION: THEREFOR	RESULT 11 US-09-726-810-2597 ; Sequence 2597, Application US/09726810 ; GENERAL INFORMATION:	2471 ATAATATTTCAGGATATTTTCCTCTACAATAAAGTAACAATTAACTTA	Db 2411 ACCAGATTGTTTGGCTAACACATCCCGAAGAATGATTTTGTCAGGAATTATTGTTATTTA 2470 OV 1861 ATAAATATTTCAGGATATTTTTCCTCTTACAATAAAGTAACTAAC
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APPLICANT: Morris, MacDonald
APPLICANT: Lal, Preeti
APPLICANT: Lal, Preeti
APPLICANT: Diep, Dinh
FITTLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
FITTLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
FITTLE OF INVENTION: Mothod Sequence Databases, and Single Nucleotide Polymor
FITTLE OF INVENTION: Identified Thereby
FILE REPERENCE: GX-0016 P
CURRENT FILING DATE: 2000-06-21
NUMBER OF SEQ ID NOS: 9429
SOFTWARE: PERL Program
SEQ ID NO 4025
LENGTH: 2087
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: 235222.9
US-60-213-362-4025
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Query Match Best Local Similarity 100.0%; Pred. No. 0; Matches 1909; Conservative 0; Pred. No. 0; Matches 1909; Conservative 0; Pred. No. 0; Matches 1909; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  Qy 1 CTTGGTCCTGATGTCTGACCATGGAGATGTGAGCCTCCGCCCGAAGACCGGGTGAGGGC 60 Db 179 CTTGGTCCTGATGTCTGACCATGGAGATGTGAGCCTCCGCCCGAAGACCGGGTGAGGGC 238  Qy 61 TCTCTCCCAGCTGGGTAGTGCGGTAGAGGTGAATGAAGAAATTCCACCCGGTCGGT	US-60-278-561-6951  (Sequence 6951, Application US/60278561  (Sequence 6951, Application US/60278561  (Sequence 6951, Application US/60278561  (Sequence 6951, Application US/60278561  (APPLICANT: Mail, Preeti APPLICANT: Diep, Dinh  TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using  TITLE OF INVENTION: Polymucleotide Sequence Databases, and Single Nucleotide  TITLE OF INVENTION: Polymorphisms Identified Thereby  FILE REPERENCE: GX-0012-1 p  CURRENT APPLICATION UNMERS: US/60/278,561  CURRENT APPLICATION UNMERS: US/60/278,561  CURRENT FILING DATE: 2001-03-23  NUMBER: PERL Program  SEQ ID NO 6951  LENGTH: 2087  TYPE: DNA  ORGANISM: Homo sapiens  FEATURE:  NAME/KEY: misc_feature  OTHER INFORMATION: Incyte ID No: 235222.9  US-60-278-561-6951	Qy 1561 GGTATAATGAACCCCCATATACCCTTCCTTCTGGATTCACCATTTTTTTC 1620
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	Db 179 CTTGGTCCTGATGTGTGACCATGGAGATGTGAAGCCTCCCGCCCG	1 CTTGGTCCTGATGTCTGACCATGGAGATGTGAGCCTCCCGGCCCGAAGACCCGGGTGAGGCC	Query Match 99.9%; Score 1909; DB 89; Length 2087; Best Local Similarity 100.0%; Pred. No. 0; Matches 1909; Conservative 0; Mismatches 0; Indels 0; Gaps	FEATURE: NAME/KEY: misc feat OTHER INFORMATION: JS-60-324-185-16983	; SEQ ID NO 16983 ; LENGTH: 2087 TYPE: DNA : ORGANISM: Homo sapiens	; FILE REFERENCE: GA-0015-1 F ; CURRENT APPLICATION NUMBER: US/60/324,185 ; CURRENT FILING DATE: 2001-09-21 ; NUMBER OF SEQ ID NOS: 35862	APPLICANT: Diep, Dinh TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS UNTITLE OF INVENTION: POLYMOCLECTIDE SEQUENCE DATABASES, AND SINGLE NUCLECTIDE TITLE OF INVENTION: POLYMORPHISMS IDENTIFIED THEREBY	; Sequence 16983, Application US/60324185 ; GENERAL INFORMATION: ; APPLICANT: Morris, MacDonald ; APPLICANT: Lal, Preeti	RESULT 14 US-60-324-185-16983	QY 1861 ATAAATATTTCAGGATATTTTTCCTCTACAATAAAGTAACAATTAACTT 1909 	Qy 1801 ACCAGATTGTTTGGCTAACACATCCCGAAGAATGATTTTTGTCAGGAATTATTGTTATTTA 186	QY 1741 TGGTTTATGGCAATATGAATGGAGGCTTATTACTGGGGTGAGGGACAGCTTACTCCATTTG 1800	QY 1681 CAATAAGGGCATCTGTGCAGAAATTTGGAAGCCATTTAGAAAATCTTTTGGATTTTCCTG 1740 	Qy 1621 CTCTCAGCTATCCTTCTAATTTCTCTAATTTCAATTTGTTTATATTTACCTCTGGGCT 1680	OY 1561 GGTATAATGAACCCCCATATACCCTTCCTGGATTCACCAATTGTTAACATTTTTTTC 1620	Oy 1501 AACTGTAACTCAGAAATTAAGTTACTCAGAAATTAAGTAGCTCAGAAATTAAGAAAGA	OY 1441 AAGAAATAACTGAACATATTTTTTAGGCAAGTCAGAAAGAGAACATGGTCACCCAAAAGC 1500 	OY 1381 TAGATAGTAGAAAGGGGGGCATCACCTGAGAAAGAGCTGATTTTGTATTTCAGGTTTGAA 1440
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CTTGGTCCTGATGTGTGACCATGGAGATGTGAGCCTCCCGGCCCGAAGACCGGGTGAGGGC 60	Y Match 29.9%; Score 1908; DB 102; Length 2091; Local Similarity 99.7%; Pred. No. 0; hes 1905; Conservative 5; Mismatches 0; Indels 0; Gaps 0;	LENCTH: 2091 TYPE: DNA ORGANISM: Homo sapiens :0-452-680-11695	Ø	OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF REFERENCE: CL001450 INT APPLICATION NUMBER: US/60/452,680	Sequence 11695, Application US/60452680 GENERAL INFORMATION: APPLICANT: CARCHILL, Michele APPLICANT: GRUPE, Andrew	SULT 15 -60-452-680-11695	ATAAATATITTCAGGATATTTTTCCTCTACAATAAAGTAACAATTAACTT 1909 	ACCAGATTGTTTGGCTAACACATCCCGAAGAATGATTTTGTCAGGAATTATTGTTATTTA 1860 	TGGTTTATGGCAATATGAATGCAGCTTATTACTGGGGTGAGGGACAGCTTACTCCATTTG 1800 	CAATAAGGGCATCTGTGCAGAAATTTGGAAGCCATTTAGAAAATCTTTTGGATTTTCCTG 1740	CTCTCAGCTATCCTTCTAATTTCTCTCTAATTTCAATTTGTTTATATTTACCTCTGGGCT 1680 	GGTATAATGAACCCCGATATACCCTTCCTTCTGGATTCACCAATTGTTAACATTTTTTTC 1620 	AACTGTAACTCAGAAATTAAGTTACTCAGAAATTAAGTAGCTCAGAAATTAAGAAAGA	AAGAAATAACTGAACATATTTTTTAGGCAAGTCAGAAAGAGAACATGGTCACCCAAAAGC 1500 	TAGATAGTAGAAAGGGGGGCATCACCTGAGAAAGAGCTGATTTTGTATTTCAGGTTTGAA 1440 	CCATATCAGTGTACTGTAGCCCCTTAATTTAAGCTTTCTAGAAAGCTTTGGAAGTTTTTG 1380 	AGTGACCATCACAGACCTTCGATGAGCGTTTGAGTCCAACACCTTCCAAGAACAACAAAA 1320 	ACACAGCAAGGATCCACCTCTGTTCTGTAGCTGCAGCCACGTGACTGTTGTGGACAGAGC 1438
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## SUMMARIES

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## ALIGNMENTS

RESULT 1
AAA59852
ID AAA5
XX AAA5
AC AAA5
XX AMSH
KW CANC
CXX HOMO
DH 13-0
XX HOMO
CXX I2-N
CANC
CX I2-N
CX I1-N
CX IN-N
CX IN-N 12-NOV-1998; 12-NOV-1999; 25-MAY-2000 WO200029436-A1. Homo sapiens. cancer; autoimmune disorder; AMSH; signal transduction; SH3 domain; cytokine; STAM; severe infection; Human AMSH nucleotide sequence. 13-OCT-2000 AAA59852; AAA59852 standard; cDNA; 1910 BP. (first entry) 98JP-00322674. 99WO-JP006309. human; ss

Sugamura K, Tanaka

(NISC-) JAPAN SCI & TECHNOLOGY CORP.

WPI; 2000-387743/33. P-PSDB; AAB03791.

Protein AMSH being signal transducer interacting with SH3 domain of cytokine signal transducer STAM, for diagnosis and development of drugs of transing diseases e.g. severe infection, cancers and autoimmune

Claim 4; Page 14-15; 22pp; Japanese.

This sequence represents the human AMSH gene. The AMSH protein is involved in signal transduction, and interacts with the SH3 domain of cytokine signal transducer STAM. The invention includes human and murine AMSH protein and gene sequences (hAMSH and mAMSH), and also includes antibodies directed against hAMSH and mAMSH. The AMSH protein can be used in the diagnosis and development of drugs for treating diseases due to the dysfunction of cytokine signal transduction e.g. severe infection, cancers and autoimmune disorders

ÖS

Sequence

1910

Query Match Best Local S Matches 1910

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                           GAAACCTGGAGCACTGAGCAACTCAGAAAGTATTCCCACAATCGATGGATTGCGCCATGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to Smad associating polypeptides (SAP) and nucleic acids encoding the SAPs. The SAPs can be expressed by standard recombinant methodology. The SAP proteins and polynucleotides are useful for regulating the cell cycle in a mammalian cell, and for modulating TGF-beta superfamily signal transduction in a mammalian cell. SAP polypeptide are useful for testing Smad binding, for testing polypeptide are useful for testing smad binding, for testing phosphorylation, for generating antibodies, and as components of an immunoassay. The SAP polynucleotides are useful in gene therapy. The present sequence represents the nucleotide sequence of human SAP1/AMSH that can be used in modulating TGF-beta superfamily signal transduction in a mammalian cell.
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17-DEC-1998;
23-JUN-1999;
The present invention describes an isolated polypeptide comprising an immunogenic portion of an ovarian carcinoma protein (or its variants). Ovarian carcinoma proteins, and polypucleotides encoding them, have cytostatic activity and can be used in gene therapy and vaccines. Ovarian
                                                                                                                                                                                                  Immunogenic portion of an ovarian carcinoma protein and the nucleic acid encoding it, useful for the diagnosis, prevention and treatment of cancer, preferably ovarian cancer.
                                                                                                                                                                                                                                                                                                                                                                          Mitcham JL,
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patient
                                                                                                                                                                                                                                                                                  This invention relates to polypeptides comprising an immunogenic portic of an ovarian carcinoma protein which acts as an immunostimulant and is cytostatic. The polypeptides, polypuclabotides, antibodies, fusion proteins, T cell populations and antigen presenting cells that express the polypeptides are useful for stimulating an immune response in a patient and treating ovarian cancer. This sequence represents DNA relation the invention
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10-AUG-2000); 2000US-00636801.

20-SEP-2000); 2000US-00667857.

04-APR-2001; 2001US-00827271.

18-JUN-2001; 2001US-00884441.
                                                                                                                                                                                                                                              Sequence 1043 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (FANG/)
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(FLIN/)
(RETT/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (KING/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-JUN-2001; 2001US-00884441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1043 BP; 313 A; 224 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           technology. The present sequence represents a human antigen polynucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CART/)
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KING G E.
ALIGATE P A.
PLING S P.
RETTER M W.
FANGER G R.
REED S G.
VEDVICK T S.
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, Vedvick
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                                                                                                           TCCAGTGTCGACCTACACACTCACTGCTCTTACCAGATGATGTTGCCAGAGTCAGTAGCC 1102
                                                                                                                                                                                                 CAGCAGGGCCTCATCACACTGGGCTGGATTCATACTCACCCCACACAGACCGCGTTTCTC
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                                  CAGCAGGGCCTCATCACACTGGGCTGGATTCATACTCACCCCACACAGACCGCGTTTCTC
            Fig
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Pred. No. 8.8e-276;
0; Mismatches 0;
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tumour antigen; identification; cytostatic; gene therapy; vaccine;
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Best Local Similarity
Matches 1040; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes an isolated polypeptide comprising an immunogenic portion of an ovarian carcinoma protein (or its variants). Ovarian carcinoma proteins, and polymucleotides encoding them, have cytostatic activity and can be used in gene therapy and vaccines. Ovarian carcinoma polypeptides, nucleic acids, antibodies and vaccines are useful for the prevention, diagnosis and treatment of cancer, preferably ovarian cancer. AAA59691 to AAA70077 and AAB12552 to AAB12557 represent human ovarian carcinoma polynucleotides and proteins used in the exemplification of the present invention
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17-DEC-1998;
23-JUN-1999;
24-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1041 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1;
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CACNTGAGAAAGAGCTGATTTTGTATTTCAGGTTTTGAAAAGAAATAACTGAACATATTTT
                                             CTTAATTTAAGCTTTCTAGAAAGCTTTGGAAGTTTTTGTAGATAGTAGAAAGGGGGGCAT
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ATTTGGAAGCCATTTAGAAAATCTTTTGGATTTTCCTGTGGTTTATGGCAATATGAATGG

Query Match Best Local Similarity

Score Pred. C; 198

1040; DB 8; No. 5.9e-275;

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Sequence 1041 BP; 312 A; 223

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                             The invention relates to an isolated 0772P polypeptide, which has the structure fully defined in the specification. The composition containing the polypeptides, polynucleotides, fusion proteins, antibodies, T-cells or antigen presenting cells are useful for stimulating an immune response and treating ovarian cancer. Detecting the presence of the polynucleotides and polypeptides is useful for diagnosing cancer. Ovarian carcinoma cDNAs and protein cDNAs were identified using microarray technology. The present sequence represents a human ovarian carcinoma antigen polynucleotides.
                                                                                                                                                                                                                                           Mitcham
Reed SG,
                        antigen
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                                                                                                                                                                               New isolated 0772P polypeptides and polynucleotides, useful in gene therapy, particularly for treating or diagnosing cancer, e.g. ovarian
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(ALGA/)
(FLIN/)
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, Vedvick
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KING G E.
ALGATE P A.
FILING S P.
RETTER M W.
FANGER G R.
REED S G.
VEDVICK T S.
                                                                                                                                                                                                                                                                             CARTER D. HILL P. ALBONE E.
                       polynucleotide.
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Best Local S
Matches 1028
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AMSH; signal transduction; SH3 domain; cytokine; STAM; severe infection; cancer; autoimmune disorder; mouse; ss.
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Protein AMSH being signal transducer interacting with SH3 domain o cytokine signal transducer STAM, for diagnosis and development of of treating diseases e.g. severe infection, cancers and autoimmune f drugs

This sequence represents the murine AMSH gene. The AMSH protein is involved in signal transduction, and interacts with the SH3 domain of cytokine signal transducer STAM. The invention includes human and murine AMSH protein and gene sequences (hAMSH and mAMSH), and also includes antibodies directed against hAMSH and mAMSH. The AMSH protein can be used in the diagnosis and development of drugs for treating diseases due to the dysfunction of cytokine signal transduction e.g. severe infection,

ATGTCTGACCATGGGGATGTGAGCCTCCCACCCCAAGACCGGGTGAGGATTCTGTCCCAA 115 ATGTCTGACCATGGAGATGTGAGCCTCCCCGCCCGAAGACCCGGGTGAGGGCTCTCTCCCAG ATCCTCTACAACAAGTACATCACGCTGTTTATTGAAAAACTTCCGAAACACCGAGACTAC ATCCTCTATAACAAGTATATCACGCTCTTTATTGAGAAACTACCAAAACATCGAGATTAC GTTGAGATCATCCGCATGGCGTCCGTTTACTCGGAAGAAGGCAACATTGAACATGCCTTT GTTGAGATTATCCGAATGGCATCCATTTACTCTGAGGAAGGCAACATTGAACATGCCTTC 190 CTTGGGAGTGCAGTTGAGTTAAATGAAGACATTCCACCCCGTCGCTACTACCGCTCCGGT CTGGGTAGTGCGGTAGAGGTGAATGAAGACATTCCACCCCGTCGGTACTTCCGCTCTGGA 130 Indels Length 1384; 0; 310 235 175 70 295 250 0

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14-JUL-2000

26-JUL-2000

14-AUG-2000

15-AUG-2000

16-SEP-2000

01-SEP-2000

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16-MAR-2000;
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17-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; nootropic; r
immunosuppressive;
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                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to novel genes (ABA11004-ABA21534) and proteins (C (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. C The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and covarian cancer and other cancers of the adrenal gland, bone, bone marrow, the reast, gastrointestinal tract, liver, lung, or urogenital; (b) immune c disorders e.g. Addison's disease, allergies, autoimmune haemolytic multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascultar disorders such as myocardial ischaemias; (d) wound healing (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from wipo at fip.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Sim:
Matches 682;
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GAAATTAAGTAGCTCAGAAATTAAGAAAGAATGGTATAATGAACCCCCATATACCCTTCC
                                                 AAGTCAGAAAGAGAACATGGTCACCCAAAAGCAACTGTAACTCAGAAATTAAGTTACTCA
                                                                                                         AGAAAGAGCTGAATTTTGTATTTCAGGTTTGAAAAGAAATAACTGAACATATTTTTTAGGC
                                                                                                                                                 TTAAGCTTTCTAGAAAGCTTTGGAAGTTTTTGTAGATAGTAGAAAGGGGGGCATCACCTG
                                                                                                                                                                                                            TTTGAGTCCAACACC
                                                                                                                                                                                                                        TTTGAGTCCAACACCTTCCAAGAACAACAAAACCATATCAGTGTACTGTAGCCCCTTAAT
                                                                                                                                                                                                                                                               AGCTGCAGCCACGTGACTGTTGTGGACAGAGCAGTGACCATCACAGACCTTCGATGAGCG
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                                                                                        agaaagagctgattttgtatttcaggtttgaaaagaaataactgaacatattttttaggc
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                                CAGAAAGAGAACATGGTCACCCAAAAGCAACTGTAACTCAGAAATTAAGTTACTCA
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21-SEP-2000
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The invention relates to isolated polynuclectide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynuclectides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food
                                                                                                                                                                                                                    New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                       Claim 1; SEQ ID NO 21022; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                         31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding
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GATCAGCAGGGCCTCATCACACTGGGCTGGATTCAT 885
                                                                        CAAAGTGCTGGGTCTGATTACTGCAACACAGAGAACGAAGAAGTTTTTCCTCATACAG
                                                                                                         ATTCTCTGTGGAAAACTGATGAGGAATGAATTTACCATTACCCATGTTCTCATCCCCAAG
                                                                                                                                                                               ATTCTCTGTGGAAAACTGATGAGGAATGAATTTACCATTACCCATGTTCTCATCCCCAAG
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Pred. No. 1.9e-163;
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RESULT 12
ABZ56929
ID ABZ56929 standard; DNA; 1621 BP.
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AC ABZ56929;
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AC ABZ56929;
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DT 04-APR-2003 (first entry)
XX
DE Human AMSH-LP DNA # SEQ ID 1.
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a cell death-inducible model non-human animal, characterised by deletion of the AMSH or/and AMSH-IP gene function on the chromosome. The model animals are applicable in screening promoters or inhibitors to treat and diagnose diseases in the nervous or immune system caused by deletion of AMSH and/or AMSH-IP. The current sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1621 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     represents a human AMSH-LP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cell death-inducing model non-human animals specifically in nervous immune system for study and analysis of cytokine signal transfer mechanism, applicable in screening promoters or inhibitors.
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DB; ABP60075.
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                  TATTTGCAAAGCAAAAACAAATATAAAGCTGAAATTCTCAAAAATTGGAGCATCAGAGA
                                                                                                            CCCAAAGCAGAAGAGCTGAAGGCAGAGCTGTTAAAACGATATACCCAAAGAATATACAGAA
                                                                                                                                                                                                                                                                                                                          GTTGAGATTATCCGAATGGCATCCATTTACTCTGAGGAAGGCAACATTGAACATGCCTTC
                                                   TATAATGAAGAAAAGAAGGAAGGAAGCAATTGGCCCGGAACATGGCCATCCAGCAA
                                                                                    CCAAGGACAGATGAATTGAAAAACGACCTTTTAAAGAAATATATAACGTAGAATACCAAGAA
                                                                                                                                                          CAGCAATGTGCAGTACCTGAAAAAGCAGGATATTATGAAGAAACTGAAGGAGATTGCATTC
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Pred. No. 1.3e-105;
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Mouse; AMSH-LP;
nervous system;
                                                 Mouse AMSH-LP DNA # SEQ ID
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DNA; 1392

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neuroprotective; immunomodulator; immune system; gene; ds.

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                                                                                       GAGCCCAGGCTGTTCAGTATATGCAAACATGTGTTGGTAAAAGACATAAAATAATTGTG
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                                                           peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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                                                                                                                                   cytostatic; gene therapy; central nervous system;
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Best Local S
Matches 730
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21-JAN-2000; 2000US-00488725.
25-APR-2000; 2000US-00552317.
20-UN-2000; 2000US-00558042.
19-JUL-2000; 2000US-00620312.
03-AUG-2000; 2000US-00633450.
14-SEP-2000; 2000US-00662191.
19-CCT-2000; 2000US-00653036.
29-NOV-2000; 2000US-00727344.
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Wang J,
Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4052 BP; 1156 A; 905 C; 910 G; 1081 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel nucleic acids and polypeptides, useful for treating as central nervous system injuries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 1770; 10078pp; English.
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1112 CAGCAATGTGCAGTACCTGAAAAGCAGGATATTATGAAGAAACTGAAGGAGATTGCATTC 1171
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Wang Z,
Goodrich
                              AAATCTGCTGTCATTCCTGAAAAGAAAGACACAGTAAAGAAATTAAAGGAGATTGCATTT
                                                                                               ATCCTCTATAACAAGTATATCACGCTCTTTATTGAGAAACTACCAAAACATCGAGATTAC
                                                              GTTCTTTATAAATTTATAACCTTATTTGTAGAAAAGCTTCCTAACCATCGAGATTAC
                                                                                                                               GTTGAGATTATCCGAATGGCATCCATTTACTCTGAGGAAGGCAACATTGAACATGCCTTC
                                                                                                                                                                                                CTTGGTTGTAATATCACCATCAGTGAAGACATCACTCCACGACGTTACTTTAGGTCTGGA
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Wehrman T,
h R, Drmanac
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Xu C,
IC RT;
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Xue AJ,
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Yang Y,
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Zhang J,
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J, Zhao QA;
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GAGCCCAGGCTGTTCAGTA
                                                                                                                                          GACCATGGACTAGAGGAGATTTCTTCCTGTCGCCAGAAAGGATTTCATCCACACAGCAAG
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                                                                                                      GAGGCCATTGCCATTGCTCACCAAAGCATAAAGACACTGGCATCTTCAGGCTCACC
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                                                                                                                                                                                                                                                                                                                             ACTGCATTTTTATCCAGCGTTGATCTTCACACTCACTGTTCCTATCAACTCATGTTGCCA
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11155.531 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd:
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Pred. No. is the number of results predicted by chance to have a

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## ALIGNMENTS

AUTHORS TITLE JOURNAL	REFERENCE	SOURCE ORGANISM	VERSION KEYWORDS	ACCESSION	RESULT 1 E35541 LOCUS
Sugamura, K. and Tanaka, N. Protein AMSH and cDNA thereof Patent: JP 2000139469-A 1 23-MAY-2000;	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1910)	Homo sapiens (human)	E35541.1 GI:18624562 JP 2000139469-A/1.	Protein AMSH and cDNA thereof. E35541	E35541 1910 bp DNA linear PAT 31-JAN-2002

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PF 12-NOV-1998 JP 1998322674
PF KAZUO SUGAMURA, NOBUYUKI TAN
PI KAZUO SUGAMURA, NOBUYUKI TAN
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1261 AGTGACCATCACAGACCTTCGATGAGGGTTTGAGTCCAACCACCTTCCAAGAACAACAAA 1		1081 GATGTTGGCAGAGTAAGTAGCCATTGTTTGGTGCCCCAAGTTCAGAAACTGGATTCTT 11	1021 CCCCACAGAGCGGGTTTCTCTCCAGTGTCGAGCTACAGACTCACTGCTCTTACCAGAT 10	QY 961 AGAACTITICCICATACAGGATCAGGGGCCTCATCACACTGGGCTGGATTCATACTCA 1020	QY 901 CCATGTTCTCATCCCCAAGCAAAGTGCTGGGTCTGATTACTGCAACACAGAGAACGAAGA 960	OY 841 GGGAGTGGAGACATGTGGAATTCTCTGTGGAAAACTGATGAGGAATGAAT	Qy 781 GGTGGTGCCTGGGCGGCTGTGCCCACAGTTTCTCCAGTTAGCCAGTGCCAACACTGCCCG 840	Qy 721 GAAACCTGGAGCACTGAGCAACTCAGAAAGTATTCCCACAATCGATGGATTGCGCCATGT 780	Qy 661 GCCTTCAGACTGTCACACAACTGTAAGGCCAGCTAAGCCACCTGTGGTGGACAAGGTCCTT 720	QY 601 GCCTGACTTGGAGAAGCCCTCCTTAGATGTGTTCCCCACCTTAACAGTCTCATCCATACA 660	GCGACTGAAAATTGTACAGGAGTTTGGGAAGGTAGACCCTGGCCTAGGTGGCCCGC	Qy 481 GGAACAGGAACAGTTCCATGCCTTCGAGGAGATGATCCGGAACCAGGAGCTAGAAAAAGA 540	Qy 421 CATCCAGCAAGAGCTGGAAAAGGAAAACAGAGGTAGCACAACAACAGCAGCAGCAGCAATT 480	361 ATATACAGAATATAATGAAGAAAAAAAAGAAGGAAGCAGAGGAATTTGGCCCGGAACATGGC 42	Qy 301 GATTGCATTTCCCAAAGCAGAAGAGCTGAAGGGGAGAGCTGTTAAAACGATATACCAAAGA 360	Qy 241 TCGAGATTACAAATCTGCTGTCATTCCTGAAAAGAAAGAA

RESULT 3 AX100575 LOCUS Sequence 1 from Pate AX100575 AX100575 AX100575 AX100575 AX100575 VERSION AX100575.1 GI:1361: XEYMORDS SOURCE Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Metazoa; Mammalia; Eutheria; AUTHORS Itoh,F., Itoh,S., H TITLE Smad associating polyonates FEATURES Source LOCATION OF ATENTITUTE FOUR Sund ASSOCIATING FOUR STITUTE FOUR Sund Sund Sund Sund Sund Sund Sund Sund	Db 1321 CCATATCAGTGTACT  Qy 1381 TAGATAGTAGAAAGG  Qy 1441 AAGAAATAACTGAAC  Qy 1441 AAGAAATAACTGAAC  Qy 1501 AACTGTAACTGAAC  Qy 1501 AACTGTAACTGAAC  Qy 1501 AACTGTAACTCAGAA  Qy 1501 AACTGTAATGAACCCC  Qy 1561 GGTATAATGAACCCC  Qy 1621 CTCTCAGCTATCCTT  Db 1621 CTCTCAGCTATCCTT  Qy 1681 CAATAAGGGCATCTG  Qy 1681 CAATAAGGGCATCTG  Qy 1741 TGGTTTATGGCAATA  Db 1741 TGGTTTATGGCAATA  Db 1741 TGGTTTATGGCAATA  Qy 1861 ATAAATATTTCAGGA  Qy 1861 ATAAATATTTCAGGA  Qy 1861 ATAAATATTTCAGGA  Db 1861 ATAAATATTTCAGGA  Db 1861 ATAAATATTTCAGGA
AX100575  Sequence 1 from Patent W00121794.  AX100575.1 GI:13619578  Homo sapiens (human)  Homo sapiens (human)  Homo sapiens  Eukaryota; Metazoa; Chordata; Craniata; Eukaryota; Metazoa; Primates; Catarrhini 1  Itoh,F., Itoh,S., Heldin,C.H. and Ten-Di Smad associating polypeptides  Patent: W0 0121794-A1 129-MAR-2001;  LUDWIG INSTITUTE FOR CANCER RESEARCH (US Location/Qualifiers 1.2003  /organism="Homo sapiens" /mol type="unassigned DNA" /db_xref="taxon:9606" 63. 1337 /note="unnamed protein product" /db_xref="exart=1" /foodon_start=1 /protein_id="CAC36455.1" /db_xref="REMPREMBL:CAC36455" /translation="MSDHGDVSLPEDRVRA RMASIYSEE(NIEHAPILYMKYITLFIEKLP AEELKAELLKRYTKYTEYTEYNEEKKKEAEELLA QFHAFEEMIRNQELEERLKIVQEEGGVDDG SDCHTTVRPAKEPPVDRSLKFGALSNSESIF RGVFTCGILCGKLMRNEFTITHVLIPXQSAG	TACTGTAGCC AAGGGGGGCA AAGGGGGGCA AAGGGGGGCA AAGGACATATIT GAAACTAATIT AGAAACTAATIT AGAAACTAATIT AGGATATATAACA AATATGAATC TCTGTGCAGA T
1 from Patent WO0121794.  1 GI:13619578  1 GI:13619578  1 GI:13619578  2 cans (human)  2 caniata; Vertebrata; Euteleostomi;  Eutheria; Primates; Catarrhini; Hominidae; Homo.  Itoh,S., Heldin,C.H. and Ten-Dijke,P.N.  2 catating polypeptides  2 catarrhini; Hominidae; Homo.  Itoh,S., Heldin,C.H. and Ten-Dijke,P.N.  2 catating polypeptides  2 catarrhini; Hominidae; Homo.  Itoh,S., Heldin,C.H. and Ten-Dijke,P.N.  2 catarrhini; Hominidae; Homo.  2 catarrhini; Hominidae; Homo.  1 catating polypeptides  2 catarrhini; Hominidae; Homo.  3 catarrhini; Hominidae; Homo.  3 catarrhini; Hominidae; Homo.  4 catarrhini; Hominidae; Homo.  5 catarrhini; Hominidae; Homo.  5 catarrhini; Hominidae; Homo.  6 catarrh	CCTTRAITTAAGCTTTCTAGAAAGCTTTTGGAAGTTTTGAA TCACCTGAGAAAGAGCTGATTTTGTATTTCAGGTTTGAA TCACCTGAGAAAGAGCTGATTTTGTATTTCAGGTTTGAA TCACCTGAGAAAGAGCTGATTTTGTATTTCAGGTTTGAA TCACCTGAGAAAGAGCTGATTTTGTATTTCAGGTTTGAA TCACCTGAGAAAGAGCTGATTTTGTATTTCAGGTTTGAA TCCCCAAGTCAGAAAGAGAAAATTAAGAAAGAA TTTAGGCAAGTCAGAAAGAGAAAATTAAGAAAGAA TTTAGGCAAGTCAGAAATTAAGAAAGAAT TCCCTTCCTTCTGGATTCACCAATTGTTAAGAAAGAAT TCCCTTCCTATTCAATTTCAATTTGTTAACATTTTTTTC TCCCTTCCTAATTTCAATTTGTTAATTTACCTCTGGGCT TCCTTCTAATTTCAATTTTGTTTATTTACCTCTGGGCT TCCTTCTAATTTCAATTTTGTTTAATTTTACCTCTGGGCT TCCTTCTAATTTCAATTTTGTTTAATTTTTCCTGGCT TCGTTCTAATTTCAATTTTAGAAAATCTTTTTGGATTTTTCCTG TCCTTCTAATTTCAATTTTAGAAAATCTTTTTGGATTTTTCCTG TCAATTTTGGAAAGCCATTTAGAAAATCTTTTTGGATTTTTCCTG TCAATTTTGGAAGCCATTTAGAAAATCTTTTTGGATTTTTCCTG TCAATTTTGGAAGCCATTTAGAAAATCTTTTTGGATTTTTCCTG TCAATTTTGGAAGCCATTTAGAAAATCTTTTTTGGATTTTTCCTG TCAATTTTTTTTTT
	ORIGIN OQUETY Match Db Db OQ
481 GGAACAG 533 GGAACAG 541 GCGACTG 541 GCGACTG 601 GCCTGAC 661 GCCTGAC 661 GCCTTCA 721 GAAACCT 721 GAAACCT 781 GGTGGTG 681 GGGAGTT 781 GGGACTT	Match Local Similari Local Similari Local Similari Local Similari Local Similari Local Similari 1000000000000000000000000000000000000

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Homo sapiens associated molecule with the SH3 domain
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                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILINI at: http://image.llnl.gov Series: IRAL Plate: 12 Row: 1 Column: 19
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 17738303.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karline,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: National Institutes of Health In
Sequencing Center (NISC),
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Submitted (11-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Eukaryota; Metazoa; Chordata; Craniata; Verrebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1933)
1 Crouse L.H., Derge, J.G.,
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                                                                                                /clone="MGC:3546 IMAGE:3619837"

/tissue type="Lymph, Burkitt ly

/clone_Tib="NIH_MGC_8"

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/gene="AMSH"
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/db_xref="MIM:606247"
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                                                                                                                                                                                                                                                 organism="Homo sapiens"

/mol_type="mRNA"
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misc_fea  ORIGIN  Query Match Best Local Matches 190  Qy 121  Db 61  Db 127  Qy 181  Db 247  Qy 241  Db 307  Qy 301  Db 367  Qy 421  Db 367  Qy 481  Db 427  Qy 481  Db 541  Db 547  Qy 661	CDS
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Qy 1261 AGTGACCATCACAGACCTTCGATGAGCGTTTGAGTCCAACACAGAACAACAAAA 1320	Db 1307 ACACAGCAAGGATCCACCTCTGTTCTGTAGCTGCAGCGAGCTGATGTGGACAGAGC 1366	- р	Db 1081 GATGTTGCCAGAGTCAGTAGCATTGTTTGCTCCCCCAAGTTCCAGGAAACTGGATTCTT 1140  1187 GATGTTGCCAGAGTCAGTAGCCATTGTTTGCTCCCCCAAGGTTCCAGGAAACTGGATTCTT 1246	QY 1021 CCCCACACAGACCGCGTTTCTCTCCAGTGTCGACCTACACTCACT	QY 961 AGAACTTTTCCTCATACAGGATCAGCAGGGCCTCATCACACTGGGCTGGATTCATACTCA 1020	OY 901 CCATGTTCTCATCCCCAAGCAAAGTGCTGGGTCTGATTACTGCAACACAGAGAACGAAGA 960	Qy 841 GGGAGTGGAGACATGTGGAATTCTCTGTGGAAAACTGATGAGGAATGAAT	Qy 781 GGTGGTGCCTGGGCGGCTGTGCCCACAGTTTCTCCAGTTAGCCAGTGCCAACACTGCCCG 840		Qy 661 GCCTTCAGACTGTCACACAACTGTAAGGCCAGCTAAGCCACCTGTGGACAGGTCCTT 720	QY 601 GCCTGACTTGGAGAAGCCCTCCTTAGATGTGTTCCCCCACCTTAACAGTCTCCATCCA	QY 541 GCGACTGAAAATTGTACAGGAGTTTGGGAAGGTAGACCCTAGGTGGCCCAGGTAGT 600	QY 481 GGĀACĀGGAĀCĀGTTCCĀTGCCTTCGĀGGĀGĀTGĀTCCGGĀĀCCĀGGĀGĀGĀĀĀĀĀĀGĀ 540	QY 421 CATCCAGCAAGAGCTGGAAAAGGAAAAACAGAGGGTAGCACAACAGAAGCAGCAGCATT 480	Qy 361 ATATACAGAATATAATGAAGAAAAGAAGAAGAAGCAGAGGAATTGGCCCGGAACATGGC 420	QY 301 GATTGCATTTCCCAAAGCAGAAGAGCTGAAGGCTGAAGACGATATACCAAAGA 360	347

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OS Homo sapiens (human)

PN JF 2002532093-A/19

ROSC 17-DEC-1998 US 09/215681,17-DEC-1998 US 09/216003 PR

23-JUN-1999 US 09/338933,24-SEP-1999 US 09/404879 PI

23-JUN-1999 US 09/338933,24-SEP-1998 US 09/404879 PI

23-JUN-1999 US 09/38933,24-SEP-1998 US 09/404879 PI

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1 (bases 1 to 1043)

Mitcham, J.L., King, G.E., Algate, P.A. and Frudakis, T.N.

Compositions and methods for the therapy and diagnosis of ovarian Patent: JP 2002532093-A 19 02-OCT-2002;
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Sequence 19
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                                                                                                                                                   1 (bases 1 to 1043)
Mitcham, J.L., King, G.E. and Algate, P.
Compositions and methods for therapy
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Patent: US 6488931-A 19 03-DEC-2002;
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Mitcham, J.L., Frudakis, T.N. and King,
Compositions and methods for therapy
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                                         TTAGGCAAGTCAGAAAGAGAACATGGTCACCCAAAAGCAACTGTAACTCAGAAATTAAGT
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                         TTAGGCAAGTCAGAAAGAGAACATGGTCACCCAAAAGCAACTGTAACTCAGAAATTAAGT
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REFERENCE
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SOURCE
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AR283624
LOCUS
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Best Local Similarity
Matches 1043; Conserv
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1 (bases 1 to 1043)
Mitcham, J.L., Frudakis, T.N. and King, G.
Compositions and methods for diagnosis
Patent: US 6528253-A 19 04-MAR-2003;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unknown
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GAGGAGATTTCTTCCTGTCGCCAGAAAGGATTTCATCCACACAGCAAGGATCCACCTCTG
                                         TCCAGTGTCGACCTACACTCACTGCTCTTACCAGATGATGTTGCCAGAGTCAGTAGCC
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Sequence 19
AX366252
AX366252.1
                                                                                                                                 Homo sapiens (human)
Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                             Mitcham, J.L., King, G.E., Fanger, G.R., Reed, S.G., VAlbone, B.
  Patent: WO 0206317-A 19 24-JAN-2002;
CORIXA CORPORATION (US)
Location/Qualifiers
1, .1043
                                                                   Compositions and methods for the therapy
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                                                           ATTIGGAAGCCATTIAGAAAATCTTTIGGATTITCCTGTGGTTTATGGCAATATGAATGG
                                                                                           CTCTCTAATTTCAATTTGTTTATATTTACCTCTGGGCTCAATAAGGGCATCTGTGCAGAA
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Compositions and methods for the therapy an
Patent: JP 2002532093-A 18 02-OCT-2002;
CORIXA CORP
OS Homo sapiens (human)
PN JP 2002232093-A/18
PD 02-OCT-2002
PF 17-DEC-1999 JP 2000588356
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23-UN-1999 US 09/33893, 24-SEP-1999 US 09/404879 PI
JENNIFER L MITCHAM, GORDON E KING, PAUL A ALGATE, TONY N ERUDAKIS
C12N15/09, A61K31/7115, A61K35/14, A61K35/76, A61K39/00, A61K39/395,
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PC A61K48/00,A61P35/00,A61P37/04,C07K14/82,C07K19/00,C12N1/15,
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Sequence 18 from patent US 6468546.
AR238036
AR238036.1 GI:27283000
                                                                                                                                            Unclassified.
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                                                        Patent: US 6468546-A 18 22-OCT-2002;
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/organism="unknown"
                                    Location/Qualifiers
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1 (bases 1 to 1041)
Mitcham, J.L., Frudakis, T.N. and King, G.B.
Compositions and methods for therapy and
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Location/Qualifiers
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40; Conservative
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Mitcham, J.L., Frudakis, T.N. and King, G.
Compositions and methods for diagnosis
Patent: US 6528253-A 18 04-MAR-2003;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                  Unknown
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Sequence 18 :
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     Fanger, G.R., Reed, S.G., Vedvi
Albone, E.
Compositions and methods for
                                           Mitcham, J.L.,
                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                             Homo sapiens
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                               Reed, S.G., 1
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                                                                      Chordata;
Primates;
                                Vedvick, T.S., Carter, D.,
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        the therapy and
                                                                      Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                          ATTTGGAAGCCATTTAGAAAATCTTTTTGGATTTTCCTGTGGTTTATGGCAATATGAATGG
                                                             CTCTCTAATTTCAATTTGTTTATATTTACCTCTGGGCTCAATAAGGGCATCTGTGCAGAA
                                                                               CTCTCTAATTTCAATTTGTTTATATTTACCTCTGGGCTCAATAAGGGCATCTGTGCAGAA
                                                                                                                                                                                  TACTCAGAAATTAAGTAGCTCAGAAATTAAGAAAGAATGGTATAATGAACCCCCATATAC
                                                                                                                                                                                                                                                                        CACNTGAGAAAGAGCTGATTTTGTATTTCAGGTTTGAAAAGAAATAACTGAACATATTTT
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/mol_type="unassigned DNJ
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54.5%;
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Pred. No. 1.4e-243;
0; Mismatches 1;
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omple ; 74	1021	1883	961	1823	901	1763
Search completed: August 23, 2004, 15:19:09 Job time : 7428 secs	1021 CTTTACAATAAAGTAACAAT 1041	-0	961 TCCCGAAGAATGATTTTGTCAGGAATTATTGTTATTTAATAAATA	1823 TCCCGAAGAATGATTTTGTCAGGAATTATTGTTAATAAATA	901 ACCTTATTACTGGGGTGAGGGACAGCTTACTCCATTTGACCAGATTGTTTGGCTAACACA 960	1763 AGCTTATTACTGGGGTGAGGGACAGCTTACTCCATTTGACCAGATTGTTTGGCTAACACA 1822

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Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Command line parameters:

-MODEL-frame+ p2n.model -DEV=xlh
-Q=/Ggn2_1/USPTO_Spool/US039831452/runat_17082004_151202_23722/app_query.fasta_1.583
-Q=/Ggn2_1/USPTO_Spool/US039831452/runat_17082004_151202_23722/app_query.fasta_1.583
-DB=Pending_Patents_NA_New -QPMT=fastap_-SUPFIX=p2n.rnpn -MINMATCH=0.1
-LOOPCIL=0 -LOOPEXI=0 -UNITS=bits -START=1 - END=-1 -MATRIX=blosum62
-TRANS=human40.dd -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -CUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXIEN=2000000000 -USER=US09831452_@CGN 1 177 @runat 17082004 151202 23722
-NCPU=6 -ICPU=3 -NO_MAAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK_100 -
-NCRUSCORES=0 -WAIT -DSPBLOCK_100 -
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   : //cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*
    //cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
    //cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
    //cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
    //cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
    //cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
    //cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
    //cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
    //cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq3:*
    //cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq3:*
    //cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq3:*
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     VS-10-021-698A-3931

VS-10-784-004-596

VS-10-784-004-1024

VS-10-784-004-224

VS-10-784-004-875

VS-10-370-715B-115

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Sequence 596, App
Sequence 1024, App
Sequence 224, App
Sequence 875, App
Sequence 115, App
Sequence 13, App
Sequence 18, Appl
Sequence 19, Appl
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LO-820-583A-1	50-592-408-10	50-582-609-10	10-820-583A-1	10-021-698A-2	60-582-609-10	10-767-701-855	-10-915-727-12	10-708-204-649	50-582-609-9095	10-779-543-14	10-767-701-1036	60-582-609-9093	10-021-698A-393	10-781-469-125	10-779-543-1480	10-021-698A-393	60-582-609-200	10-779-543-1296	10-021-698A-3932	-US03-41766A-427	-US03-41761-427	-US03-41761-4271	10-779-543-15310	10-425-115-1265	10-425-115-93781	10-425-115-1641	10-793-479-2838	10-425-115-126	09-404-520B-2297	10-767-701-870	10-779-543-395	09-404-520B-563	15-13930	10-425-115-1265	7-701-1373
equence 16, App	equence 104	equence 100, Ap	equence 15, App	nce 254	equence 101, Ap	equence 8559, Ap	equence 12207,	equence 6499, A	equence 90954,	equence 1	equence 10361,	equence 90937,	equence 3938, Ā	equence 125, Ap	equence 14802,	equence 3936, A	equence 200	equence 12962,	equence 3932, A	equence 42714,	equence 42714,	equence 42714,	equence 15310	equence 126535,	equence 93781,	equence 164175,	equence 2838,	equence 126538,	equence 22974,	equence 8700, A	equence 3954, A	equence 5634, A	uence 13930,	equence 126539,	equence 1373

## ALIGNMENTS

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APPLICANT: SIMON, JASON
APPLICANT: ALLEN, KRISTINA
APPLICANT: PANDIT, SINIL
APPLICANT: PANDIT, SINIL
INTIL OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES RELATING TO
FILE REFERENCE: 2976-4044US1
CURRENT APPLICATION NUMBER: US/10/021,698A
CURRENT APPLICATION NUMBER: US/10/021,698A
CURRENT FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: 60/211,749
PRIOR PRIOR APPLICATION NUMBER: 60/211,749
PRIOR PRIOR DATE: 2000-06-14
NUMBER OF SEQ ID NOS: 6160
SOFTWARE: PARIORLE 1005: 6160
SOFTWARE: PARIORLE 1005: 6160
                    Percent Similarity:
Best Local Similarity:
                                                             Score:
                                                                                                                                                      US-10-021-698A-3931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-021-698A-3931/c ; Sequence 3931, Application US/10021698A ; GENERAL INFORMATION:
  Query Match:
                                                                                      Pred. No.:
                                                                                                           Alignment Scores:
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APPLICANT: LITTLE, RANDALL
APPLICANT: VAN BERDEWECH, PAUL
APPLICANT: DUPUIS, JOSEE
TOTANT: DUPUIS, JOSEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ValGluIleIleArgMetAlaSerIleTyrSerGluGluGlyAsnIleGluHisAlaPhe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GluLysProSerLeuAspValPheProThrLeuThrValSerSerIleGlnProSerAsp
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GENERAL INFORMATION:
APPLICANT: Bicgen Idec
TITLE OF INVENTION: Surrogate Markers of Pai
TITLE OF INVENTION: Surrogate Markers of Pai
CURRENT APPLICATION NUMBER: US/10/784,004
CURRENT FILING DATE: 2004-02-20
NUMBER OF SEQ ID NOS: 1251
SOFTWARE: Patentin version 3.2
SEQ ID NO 596
LENGTH: 2107
TYPE: DNA
ORGANISM: human
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Sequence 1024, Application US/10784004
(GENERAL INFORMATION:
APPLICANT: BLOGEN Idea
TITLE OF INVENTION: Surrogate Markers of Pair FILE REFERENCE: 08201.6029.00000
CURRENT APPLICATION UNMBER: US/10/784,004
CURRENT FILING DATE: 2004.02-20
UNMBER OF SEQ ID NOS: 1251
SOFTWARE: Patentin version 3.2
SEQ ID NO 1024
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US-10-784-004-1024
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Sequence 224, Application US/10784004
GENERAL INFORMATION:
APPLICANT: Biogen Idec
FITTLE OF INVENTION: Surrogate Markers of Pain
FILE REFERENCE: 09201.6029-00000
CURRENT APPLICATION NUMBER: US/10/784,004
CURRENT FILING DATE: 2004-02-20
NUMBER OF SEQ ID NOS: 1251
NUMBER OF SEQ ID NOS: 1251
SOFTWARE: Patentin version 3.2
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              ATCCTCTACAACAAGTACATCACGCTGTTTATTGAAAAACTTCCAAAACACCGAGACTAC
                                  IleLeuTyrAsnLysTyrIleThrLeuPheIleGluLysLeuProLysHisArgAspTyr
                                                                         GTTGAGATCATCCGCATGGCATCCATTTACTCTGAAGAAGGCAACATTGAACATGCCTTT
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                                                                                                          AspProProLeuPheCysSerCysSerHisValThrValValAspArgAlaValThrIle 420
                                                                                                                                                    GACTATGGCCTTCAAGAGATTTCAACCTGCCGGCAGAAAGGCTTTCACCCCCATGGCAGA
                                                                                                                                                                      AspHisGlyLeuGluGluIleSerSerCysArgGlnLysGlyPheHisProHisSerLys
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Sequence 875, Application US/10784004

GENERAL INFORMATION:

APPLICANT: Biogen Idec

FILE OF INVENTION: Surrogate Markers of Pai

FILE REFERENCE: 08201.6029-00000

CURRENT APPLICATION NUMBER: US/10/784,004

CURRENT FILLING DATE: 2004-02-20

NUMBER OF SEQ ID NOS: 1251

SOFTWARE: PatentIn version 3.2

SEQ ID NO 875

LENGTH: 1.544

TYPE: DNA

ORGANISM: rat

US-10-784-004-875
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                                                                            GAAAAGCCCTGTGTAGATGTGGCCCCCCAGTTCACCTTTCTCGCCCACGCAGACTTCAGAC
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           TGTAACACAACCCTGAGGCCAAGCCAAGCTGTGGTGGACAGGTCCCTCAAACCTGGA
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APPLICANT: BRISDELL, HUNTE
APPLICANT: SCHOENFELD, JILL R.
APPLICANT: SCHOENFELD, JILL R.
APPLICANT: SCHOENFELD, JILL R.
APPLICANT: WILLIAMS, P. MICKEY
APPLICANT: WOOD, WILLIAMS, P. MICKEY
APPLICANT: WU, THOMAS D.
TITLE OF INVENTION: Compositions and Methods for
TITLE OF INVENTION: Related Diseases
FILE REFERENCE: P1948R1-US
CURRENT APPLICATION NUMBER: US/10/370,715B
CURRENT APPLICATION NUMBER: US/10/370,715B
UMBER OF SEQ ID NOS: 742
LENGTH: 4052
TYPE: DNA
ORGANISM: Homo sapien
US-10-370-715B-115
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Pred. No.:
         Best Local Similarity:
Query Match:
DB:
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US-10-370-715B-115
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Length:
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                                                                                        ACTATTACCCATGTAATTGTGCCAAAGCAGTCTGCGGGACCAGACTATTGTGACATGGAG
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RESULT 7
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Best Local Similarity:
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SEQ ID NO 3934
LENGTH: 1123
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APPLICANT: KEITH, TIM
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PRIOR FILING DATE: 2000-06-14
NUMBER OF SEQ ID NOS: 6160
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CURRENT APPLICATION NUMBER: US/10/021,698A
CURRENT FILING DATE: 2001-10-22
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VAN EERDEWEGH, PAUL
DUPUIS, JOSEE
DEL MASTRO, RICHARD
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ALLEN, KRISTINA
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RESULT 8
US-10-860-790-18
US-10-860-790-18
Sequence 18, Application US/10860790
REMERAL INFORMATION:
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
APPLICANT: Hill, Paul
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CAN
FILE REFERENCE: 210121.462C11
CURRENT APPLICATION NUMBER: US/10/860,790
CURRENT APPLICATION NUMBER: US/10/860,790
CURRENT FALING DATE: 2004-06-02
NUMBER OF SEQ ID NOS: 624
SOFTWARE: FASTSEQ FOR Windows Version 4.0
SEQ ID NO 18
SEQ ID NO 18
LENGTH: 1041
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
COTHER INFORMATION: n = A,T,C or G
US-10-860-790-18
                                                                                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                    US-09-831-452-1 (1-424) x US-10-860-790-18 (1-1041)
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; GENERAL INFORMATION:
; APPLICANT: Bengur, Chaitanya S.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Fill, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CAI
; FILE REFERENCE: 210121.462C11
; CURRENT APPLICATION NUMBER: US/10/860,790
; CURRENT APPLICATION DATE: 2004-06-02
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 19
LENGTH: 1043
TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                GlnGlnGlyLeuIleThrLeuGlyTrpIleHisThrHisProThrGlnThrAlaPheLeu 344
                                                                                                                                                                                                      SerAlaGlySerAspTyrCysAsnThrGluAsnGluGluGluLeuPheLeuIleGlnAsp 324
                                                                                                                                                                                                                                          CTCTGTGGAAAACTGATGAGGAATGAATTTACCATTACCCATGTTCTCATCCCCAAGCAA
                                                                                                                                                                                                                                                              LeuCysGlyLysLeuMetArgAsnGluPheThrIleThrHisValLeuIleProLysGln 304
                                                                                                               CAGCAGGGCCTCATCACACTGGGCTGGATTCATACTCACCCCACACAGACCGCGTTTCTC
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                                                TCCAGTGTCGACCTACACACTCACTGCTCTTACCAGATGATGTTGCCAGAGTCAGTAGCC
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344	Qy  47 AlaSerTleTyrSerGluGluGlyAsnIleGluHisAlaPheIleLeuTyrAsnLysTyr 66	US-09-831-452-1 (1-424) x US-10-767-701-13735 (1-1972)  Qy	No.: 4.34e-47 Length: Similarity: 45.848 Conservative: Similarity: 31.538 Mismatches: Similarity: 33.968 Gaps:	; NAME KEY: unsure; NAME KEY: unsure; OCCATION: (1)(1972); OCTHER INFORMATION: unsure at all n locations; FEATURE: OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS9218_1 US-10-767-701-13735		Sequence 13735, Application US/10767701 ; Sequence 13735, Application US/10767701 ; GENERAL INFORMATION: ; APPLICANT: Kovalic, David K. ; APPLICANT: Chou, Yihua ; APPLICANT: Cao, Yongwei ; APPLICANT: Cao, Yongwei ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With ; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement ; FILE REFERENCE: 38-21(53535)B	241 ATTG 385 GluG      301 GAGG 405 PheC      361 TTCT
. & & & & & & & & & & & & & & & & & & &	7 & B & B &	S & & & & &	0 0 0 0 0 0 0	ob da da	B & B &	OY OY Db	\$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$
		276 AlaargGlyValGluThrCysGlyIleLeuCysGlyLysLeuMetArgAsnGluPheThr 295	239 ProGlyAlaLeuSerAsnSerGluSerIleProThrIleAspGlyLeuArg 255	225	ATCTTGAACCAAGATGATTGGCATGGTGCAGTTCTCTCTC	GlyLysValAspPro	

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APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules of INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 126539
LENGTH: 2559
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Query Match:
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ORGANISM: Zea mays
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   ---ValGlnGluPheGlyLysValAspPro---GlyLeuGlyGly---
                                                 GTGGCATCATTATCGAGTGTACAGAAACAATTTATGAATCTACCATATCCAAAAGAAGAA 1036
                                                                                                                                             ArgValAlaGlnGlnLysGlnGlnGlnGlnGlnGlnGlnFheHisAlaPheGluGlu
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                                                                                                                 ACATTTGTAGGCAGCAGTAATGGAGCATTG----CAAAAACCCTTCCATGCTGGGAGACAA
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Sequence 13930, Application US/10425115
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
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Percent Similarity:
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TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 13930
LENGTH: 1660
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LOCATION: (1)...(1660)
OTHER INFORMATION: unsure at
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ORGANISM: Zea mays
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                                                                         ArgLeuLys11eValGlnGluPheGlyLysValAspProGlyLeuGlyGlyProLeuVal
                                                                                                     GCAGATGAACCTAATGGTGTATATGGAACCTATGCTGCAAGTAGTGAGTTGGAGCACCAT
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; Sequence 5634, Application US; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory
; APPLICANT: McIninch, James
; APPLICANT: McIninch, James
; APPLICANT: Yu, Jaehyuk
; APPLICANT: Yu, Jaehyuk
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APPLICANT: Yu, Jaehyuk
APPLICANT: Ghodssi, Azita
FILE REFERENCE: 38-10(15498)A
CURRENT APPLICATION NUMBER: US/09/404,520B
CURRENT FILING DATE: 1999-09-23
NUMBER OF SEQ ID NOS: 44345
SEQ ID NO 5634
LENGTH: 8639
TYPE: DN"
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Oy  174LeuGluLysGluArgleu	138 6949 148 7009 162 7069 162 7129	Qy 67 eThrLeuPhelleGluLysLeuProLysHisArgAspTyrLysSerAlaVali 85 6709 TCAATTAGTGCTTCATTTAGCCGACCATCCAGACTTGAAGGATGGGAAAGATGTGAG 6768  Qy 85 eProGluLysLysAspThrValLysLysLeuLysGluIleAlaPheProLysAl 103	Alignment Scores:  Pred. No.:  4.39e-39  Matches: 150  Conservative: 71  Best Local Similarity: 28.57% Query Match: 173  Query Match: 5  Score: 173  Query Match: 173  Query M
PRIOR FILING DATE: 1998-12-21  PRIOR FILING DATE: 1997-12-23  PRIOR APPLICATION NUMBER: 60/060,664  PRIOR APPLICATION NUMBER: 60/050,664  PRIOR FILING DATE: 1998-04-03  PRIOR PILLING DATE: 1998-10-21  PRIOR PILLING DATE: 1998-10-21  PRIOR PILLING DATE: 2000-644-10  PRIOR APPLICATION NUMBER: 60/072,910  PRIOR APPLICATION NUMBER: 60/072,910  PRIOR APPLICATION NUMBER: 60/072,910  PRIOR FILING DATE: 1998-01-28  PRIOR PILLING DATE: 1998-01-28  PRIOR APPLICATION NUMBER: 60/072,910  PRIOR APPLICATION NUMBER: 60/075,954  PRIOR APPLICATION NUMBER: 60/075,954	Qy 397 roHisSerLys 400	Qy 320 heLeuIleGlnAspGlnGlyLeuIleThrLeuGlyTrpIleHisThrHisProThrG 340	Qy 220 spCysHisThrThrValArg

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Percent Similarity:
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DB:
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PRIOR FILING DATE: 1998-03-31
Remaining Prior Application data removed -
NUMBER OF SEQ ID NOS: 23767
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3954
LENGTH: 730
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                                                                                                                               roThrGlnThrAlaPheLeuSer-SerValAspLeuHisThrHisCysSer-TyrGlnMe
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                            PhePheLysLeuThrAsp 381
                                                        TATGTTGCCAAGAAGCCNATTGGCCATTTNTTGGCTCACCAAAAGCNTAAAGACACTGGC
                                                                                                             CTACTCAAACTGCATTTTTATCCANCCGTTGATCTTTACACTCACTGNNCCTTATCAACT
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Sequence 8700, Application US/10767701

GENERAL INFORMATION:
APPLICANT: Chou, Yihua
APPLICANT: Chou, Yihua
APPLICANT: Chou, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
TITLE REFERENCE: 38-21(3535)B

FILE REFERENCE: 38-21(3535)B

CURRENT APPLICATION NUMBER: US/10/767,701

CURRENT FILING DATE: 2004-01-29

NUMBER OF SEQ ID NOS: 63128

SEQ ID NO 8700

LENGTH: 909
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ORGANISM: Sorghum
FEATURE:
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ATCTATGAGCATTGCTCCCATGTA
                          LeuPheCysSerCysSerHisVal
                                                                                     IleSerSerCysArgGlnLysGlyPheHisProHisSerLys-----AspProPro
                                                                                                                     ACGGATACAAGAAAACATĠĠĊATAŤŤŤCATĊŤĊÁĊĠGAGCCATGTĠĠĊATGGGCGTG
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                                                          ATCCATGATTGTGATGCGACTGGATTCCACCCTCATGAGGAGCCCCTAGATGGGACACCA
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Search completed: August 23, 2004, 23:10:11 Job time : 496 secs

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Result
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-MODEL-frame+ p2n.model -DEV=xlh
-Q=/Ggn2_1/USPTO_Spool/US09831452/runat_17082004_151158_23630/app_query.fasta_1.583
-DB=N Geneseq_29Jan04 -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -HANFIX=blosum62 -TRANS-human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -QUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09831452 @CGN 1 1 470 @runat 17082004 151158 23630 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEGSCORES=0 -WAIT -DSPBLOKE=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THEADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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## ALIGNMENTS

## RESULT 1 AAA59852 ID AAA5 XX AAA5 AC AAA5 XX Huma XX Huma XX AMSH KW CANC COS HOMC XX WO20 XX W020 XX HOMC XX II-N XX II-N XX II-N XX II-N XX III-N XX III-N XX III-N XX III-N XX III-N XX IIII-N XX Human AMSH nucleotide sequence cancer; autoimmune disorder; human; ss 13-OCT-2000 AAA59852; AAA59852 standard; cDNA; 1910 BP (first entry)

AMSH; signal transduction; SH3 domain; cytokine; STAM; severe infection;

Homo sapiens.

WO200029436-A1.

25-MAY-2000

12-NOV-1999; 99WO-JP006309.

12-NOV-1998; 98JP-00322674.

(NISC-) JAPAN SCI & TECHNOLOGY CORP

Sugamura K, Tanaka N;

WPI; 2000-387743/33. P-PSDB; AAB03791.

Protein AMSH being signal transducer interacting with SH3 domain of cytokine signal transducer STAM, for diagnosis and development of drugs

300 910

850 280 790

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Alignment
Pred. No.:
Score:
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transduction; phosphorylation; gene therapy; human; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to Smad associating polypeptides (SAP) and nucleic acids encoding the SAPs. The SAPs can be expressed by standard recombinant methodology. The SAP proteins and polynucleotides are useful for regulating the cell cycle in a mammalian cell, and for modulating TGF beta superfamily signal transduction in a mammalian cell. SAP polypeptide are useful for testing Smad binding, for testing phosphorylation, for generating antibodies, and as components of an immunoassay. The SAP polynucleotides are useful in gene therapy. The present sequence represents the nucleotide sequence of human SAP1/AMSH that can be used in modulating TGF-beta superfamily signal transduction in a mammalian cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a cell death-inducible model non-human anime characterised by deletion of the AMSH or/and AMSH-LP gene function of chromosome. The model animals are applicable in screening promoters inhibitors to treat and diagnose diseases in the nervous or immune scaused by deletion of AMSH and/or AMSH-LP. The current sequence represents a human AMSH-LP gene fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cell death-inducing model non-human animals specifically in nervimmune system for study and analysis of cytokine signal transfer mechanism, applicable in screening promoters or inhibitors.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a cell death-inducible model non-human animal, characterised by deletion of the AMSH or/and AMSH-LP gene function on tohromosome. The model animals are applicable in screening promoters or inhibitors to treat and diagnose diseases in the nervous or immune syst caused by deletion of AMSH and/or AMSH-LP. The current sequence represents a mouse AMSH-LP gene fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cell death-inducing model non-human animals specifically in nervous immune system for study and analysis of cytokine signal transfer mechanism, applicable in screening promoters or inhibitors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 26; Page 54-57; 68pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a cell death-inducible model non-human animal, characterised by deletion of the AMSH or/and AMSH-LP gene function on the chromosome. The model animals are applicable in screening promoters or inhibitors to treat and diagnose diseases in the nervous or immune system caused by deletion of AMSH and/or AMSH-LP. The current sequence represents a mouse AMSH-LP gene fragment
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immunosuppressive; antiulcer; ophthalmological; vulnerary; gout; anticonvulsant; cerebroprotective; nootropic; antiponvulsant; cerebroprotective; nootropic; antiponvulsant; cerebroprotective disorder; arteriosclerosis; antibacterial; cell proliferative disorder; arteriosclerosis; psoriasis; immune system disorder; inflammation;
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                  Addison's disease, adult respiratory distress syndrome, allergies, CC cirrhosis, disbetes mellitus, gout, Graves' disease, multiple sclerosis, CC cirrhosis, osteoporosis, rheumatoid arthritis, systemic lupus CC osteoarthritis, osteoporosis, rheumatoid arthritis, systemic lupus CC erythematosus, ulcerative colitis and haematopoietic cancer) a neurological disorder (e.g., stroke, epilepsy, Huntington's disease, CC Parkinson's disease, meningitis, prion diseases including kuru, CC Parkinson's disease, cerebral palsy, myasthenia gravis, diabetic neuropathy and Alzheimer's disease). Sptm sequences can be used to detect CC neuropathy and Alzheimer's disease). Sptm sequences can be used to detect CC the presence of or quantifying the amount of sptm-related polymuclectide in a sample. The sptm polymuclectide is used to design probes useful in CC diagnostic assays carried out to detect or confirm conditions, disorders, or diseases associated with abnormal levels of sptm expression. Sptm, its fragments or oligonuclectides derived from sptm may be used as primers in amplification steps prior to hybridisation. The present sequence CC represents the human sptm (101978.1) cDNA sequence of the invention
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Bratcher SR, D
                                                                                                                                                                                                                                                                                                                                                                                                                                                          recombinant techniques, the protein may be used to generate anti-sptm antibodies which may be used to analyse protein expression levels in different tissues. The sptm colecules are useful for diagnostic and therapeutic purposes e.g., to diagnose or treat a condition associated with cell signaling such as a cell proliferative disorders (e.g., arteriosclerosis, atherosclerosis, psoriasis, cancers), immune system disorders (e.g., inflammation, acquired immunodeficiency syndrome (AIDS), additions of adults are arteriosclerosis and account of the syndrome allocation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            secretory polynucleotides (sptm) with similarity to signa or transmembrane domain (TM) consensus sequences. The pol sequences of the invention are useful for producing sptm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel secretory polynucleotide (sptm) and polypeptides encoded by sptm, useful for diagnosing and treating disorders or diseases associated with cell signaling e.g., allergy, psoriasis, Grave's disease, epilepsy.
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05-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention relates to novel cDNA molecules encoding isolated secretory polynucleotides (sptm) with similarity to signal peptide (or transmembrane domain (TM) consensus sequences. The polynucleotide
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21-JAN-2000;
21-JAPR-2000;
25-APR-2000;
20-JUN-2000;
19-JUL-2000;
03-GEG-2000;
The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM4213) with nootropic, immunosuppressant and cytostatic activity. The polypuclectides are useful in gene therapy. A composition containing a polypeptide or polynuclectide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
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19-OCT-2000;
29-NOV-2000;
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  ArgHisValValValProGlyArgLeuCysProGlnPheLeuGlnLeuAlaSerAlaAsn
                                             AGGGCCTTAACGCCAGCTGCTACTCTAAGTGCTGCTTCAGAATTTAGTGGTTGAAGGACTG
                                                                                  ArgSerLeuLysProGlyAlaLeuSerAsnSerGluSerIleProThrIleAspGlyLeu
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The invention describes an isolated prostate specific polypeptide (I) nucleic acid (II) encoding it and are useful for diagnosing and monitoring the presence and metastases of prostate cancer in a patien (I), (II) and an antibody to (II) are useful in quantitative and qualitative diagnostic assays and methods for detecting, diagnostic, monitoring, treating, staging and predicting cancers in humans having cancer or may have the risk of developing cancer. (I) and (II) are all
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useful: for determining non-cancerous prostate disease, by measuring their expression levels and/or structural alterations; for determining the sample that has prostate tissue-like characteristics or is a prostate tissue, as an element in an array or a multi-analyte test to recognise expression patterns associated with prostate cancer and other prostate related disorders; and as elements in a computer program for pattern recognition of prostate disorders. (I) and (II) are useful for producing transgenic animals and cells and also in gene therapy. This sequence represents a prostate specific nucleic acid described in the

0 U; 0 Other;

931 20

ValGluIleIleArgMetAlaSerIleTyrSerGluGluGlyAsnIleGluHisAlaPhe LeuGlySerAlaValGluValAsnGluAspIleProProArgArgTyrPheArgSerGly CTTGGTTGTAATATCACCATCAGTGAAGACATCACTCCACGACGTTACTTTAGGTCTGGA

> 991 40

LysSerAlaVallleProGluLysLysAspThrValLysLysLeuLysGluIleAlaPhe GTTCTTTATAATAATTTATAACCTTATTTGTAGAAAAGCTTCCTAACCATCGAGATTAC 100 1111

TyrAsnGluGluLysLysLysGluAlaGluGluLeuAlaArgAsnMetAlaIleGlnGln 140

GluLeuGluLysGluLysGlnArgValAlaGlnGlnLysGlnGlnGlnLeuGluGlnGln TATTTGCAAAGCAAAAACAAATATAAAGCTGAAATTCTCAAAAAATTGGAGCATCAGAGA 1351 160 1291

GlnPheHisAlaPheGluGluMetIleArgAsnGlnGluLeuGluLysGluArgLeuLys 180 1411

GluLysProSerLeuAspValPheProThr-------LeuThrValSer SerIleGlnProSerAspCysHisThrThrValArgProAlaLysProProValValAsp GATGGGAGCGCTTTGTCCTGTTTTCCACACACCAGAACAATTCCTTGCTGAATGTATTT IleValGlnGluPheGlyLysValAspProGlyLeuGlyGlyProLeuValProAspLeu CTGTCAGAGCAGATT 1444 200

GCAGATCAACCTAATAAAAGTGATGCAACCAATTATGCTAGCCACTCTCCTCCTGTAAAC 1564 1504

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                                                                                           New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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Best Local Similarity:
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                                                                                   US-09-831-452-1 (1-424) x AAS85218 (1-1236)
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                                      102 LysalaGluGluLeuLysalaGluLeuLysargTyrThrLysGluTyr------
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Š В Ş В Ş 밁 5 В S 뮍 δ 밁 8 뮍 Š 밁 Ş В 592 238 532 472 198 412 178 352 292 652 258 218 158 232 GlyValGluThrCysGlyIleLeuCysGlyLysLeuMetArgAsnGluPheThrIleThr ThrGluTyrAsnGlu---GluLysLysGluAlaGluGluLeuAlaArgAsnMetAla ValValProGlyArgLeuCysProGlnPheLeuGlnLeuAlaSerAlaAsnThrAlaArg LysProGlyAlaLeuSerAsnSerGluSerIleProThrIleAspGlyLeuArgHisVal ProSerAspCysHisThrThrValArgProAlaLysProProValValAspArgSerLeu ProAspLeuGluLysProSerLeuAspValPheProThrLeuThrValSerSerIleGln ArgLeuLysIleValGlnGluPheGlyLysValAspProGlyLeuGlyGlyProLeuVal GAACAGGAACAGTTCCATGCCTTCGAGGAGATGATCCGGAACCAGGAGCTAGAAAAAGAG GluGlnGluGlnPheHisAlaPheGluGluMetIleArgAsnGlnGluLeuGluLysGlu ATCCAGCAAGAGCTGGAAAAGGAAAAACAGAGGGTAGCACAACAGAAGCAGCAGCAATTG IleGlnGlnGluLeuGluLysGluLysGlnArgValAlaGlnGlnLysGlnGlnLeu ACCAACTGGGATGACATGGAGAAGAAGAAGGAAGCAGAGGAATTGGCCCGGAACATGGCC GTGGTGCCTGGGCGGCTGTGCCCACAGTTTCCTCCAGTTAGCCAGTGCCAACACTGCCCGG AAACCTGGAGCACTGAGCAACTCAGAAAGTATTCCCACAATCGATGGATTGCGCCATGTG CCTTCAGACTGTCACAACTGTAAGGCCAGCTAAGCCACCTGTGGTGGACAGGTCCTTG CGACTGAAAATTGTACAGGAGTTTGGGAAGGTAGACCCTGGCCTAGGTGGCCCGCTAGTG 137 297 257 591 237 531 217 197 177 157 159 471 411 351 711 277 291

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21-JAN-2000;
25-APR-2000;
20-JUN-2000;
19-JUL-2000;
The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polypucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
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14-SEP-2000;
19-OCT-2000;
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                                                                                                                                           The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABIG1676-ABIG1676-ABIG1677), expressed DNA sequences (ABIG1840-ABIG1675) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                     Sequence 1611
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                       The invention discloses a polynucleotide comprising a sequence selected from 1970 fully defined nucleotide sequences which encode novel polypeptides. Also claimed is a polypeptide encoded by the polynucleotide or its partial peptide, an antibody binding to the polypeptide or peptide of the polynucleotide, immunologically assaying the polypeptide or peptide of the polynucleotide by contacting the polypeptide or peptide peptide of the polynucleotide by contacting the polypeptide or peptide with the antibody of the encoded protein, and observing the binding with the antibody of the encoded protein, and observing the binding
                                                                                                                                                                                                                                                                                                                                        New polynucleotides and polypeptides, useful for developing a diagnostic marker or medicines for regulation of their expression and activity, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isogai T,
Yamamoto J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T, Sugiyama T, o J, Isono Y, I Yoshikawa T,
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Hio Y, Otsuka K, Nagai
Otsuka M, Nagahari K, N
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     carrying the polynucleotide
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                                                                                  cc expressible manner and an antisense polynucleotide. The oligonucleotide cis useful as a primer for synthesising the polynucleotide, or as a probe complete the color of detecting the polynucleotide. The polynucleotides and encoded composed the polynucleotide of the polynucleotide the polynucleoti
BP;
540 A; 372 C;
403 G; 583 T; 0 U; 0 Other;
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# Sequence 1898

Alignment Pred. No.:

Scores:

No.:

Score:

Query Match: DB:

Percent Similarity: Best Local Similari

Similarity:

8.87e-64 815.50 69.08% 51.64% 36.93%

1898 157 53 79 15

Indels: Gaps: Mismatches: Conservative:

US-09-831-452-1 (1-424) x ADB61940 (1-1898)

LeuPro 360	$Thr \verb AlaPheLeuSerSerValAspLeuHisThrHisCysSerTyrGlnMetMetLeuPro $	341	S
CACTCAA 1382	AATGTTCAGGATCAACATGATCTCCTCACTCTAGGATGGAT	1323	Фd
oThrGln 340	LeuIleGlnAspGlnGlnGlyLeuIleThrLeuGlyTrpIleHisThrHisProThrGln	321	Ş
ATTATTC 1322	GTGCCAAAGCAGTCTGCGGGACCAGACTATTGTGACATGGAGAATGTAGAGGA	1263	ρb
LeuPhe 320	IleProLysGlnSerAlaGlySerAspTyrCysAsnThrGluAsnGluGluGluEuphe	301	γQ
TGTAATT 1262	ACCTGTGGAATACTCTGTGGAAAACTGACACATAATGAATTTACTATTACCCA	1203	Ь
sValLeu 300	ThrCysGlyIleLeuCysGlyLysLeuMetArgAsnGluPheThrIleThrHisValLeu	281	δδ.
AATAGAA 1202	GAAGATCTTTGCCACAAATTTCTGCAACTGGCAGAATCTAATACAGTGAGAGGG	1143	Дb
ValGlu 280	GlyArgLeuCysProGlnPheLeuGlnLeuAlaSerAlaAsnThrAlaArgGlyValGlu	261	Qy
TTTGCCA 1142	GCTACTCTAAGTGCTGTTCAGAATTTAGTGGTTGAAGGACTGCGATGTGTAGT	1083	Дb
ValPro 260	AlaLeuSerAsnSerGluSerIleProThrIleAspGlyLeuArgHisValValValPro	241	Qy
SCCAGCT 1082	AGTGATGCAACCAATTATGCTAGCCACTCTCCTGCTAAACAGGGCCTTAACC	1023	рb
sProGly 240	CysHisThrThrValArgProAlaLysProProValValAspArgSerLeuLysProGly	221	Qy
TAATAAA 1022	TGCTTTTCCACACCAGAACAATTCCTTGCTGAATGTATTTGCAGATCAACC	963	ర్జ
oSerAsp 220 	ValPheProThrLeuThrValSerSerIleGlnProSerAsp	207	Qy
TTTGTCC 962	CTGTCAGAGCAGATTGATGGGAGCGCTTTGTCC	930	Дb
rLeuAsp 206	LysValAspProGlyLeuGlyGlyProLeuValProAspLeuGluLysProSerLeuAsp	187	δÃ
CTCAGGG 929	GATCAACTCAAGAAGCAAGAGTTAGCCCGAGGTCAAATGCGAAGTCAGCAAACC	870	В
uPheGly 186	GluMetIleArgAsnGlnGluLeuGluLysGluArgLeuLysIleValGlnGluPheGly	167	ργ
TTTCGAA 869	AAGCGGATTGCTCAGATGCGCCAGCAGCAGCTAGAATCGGAGCAGTTTCTGTTT	810	Дb
aPheGlu 166	GlnArgValAlaGlnGlnLysGlnGlnGlnGlnGlnGlnGlnGlnPheHisAlaPheGlu	147	Ş
AGAAAGG 809	AAATATAAAGCTGAAATTCTCAAAAAATTGGAGCATCAGAGATTGATAGAGGC	750	ф
sGluLys 146	LysGluAlaGluGluLeuAlaArgAsnMetAlaIleGlnGlnGlnLeuGluLysGluLys	127	Ş

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RESULT 14
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ID AAA69
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XX IT-DE
PR 17-DE
PR 17-DE
PR 17-DE
PR 23-JU
PR 23-JU
PR 24-SE
XX IT-DE
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XX IT-DE
PR 23-JU
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  Percent Similarity:
                                                                                                                                                              The present invention describes an isolated polypeptide comprising an immunogenic portion of an ovarian carcinoma protean (or its variants). Ovarian carcinoma proteins, and polypucleotides encoding them, have cytostatic activity and can be used in gene therapy and vaccines. Ovarian carcinoma polypeptides, nucleic acids, antibodies and vaccines are useful for the prevention, diagnosis and treatment of cancer, preferably ovarian cancer. AAA69691 to AAB10177 and AAB12552 to AAB12557 represent human ovarian carcinoma polynucleotides and proteins used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunogenic portion of an ovarian carcinoma protein and the nuceencoding it, useful for the diagnosis, prevention and treatment cancer, preferably ovarian cancer.
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17-DEC-1998;
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99US-00338933.
99US-00404879.
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Matches:
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                                                                                          Mitcham JL, King
Reed SG, Vedvick
                                                                                                                                            17-JUL-2000; 2000US-00617747; 10-AUG-2000; 2000US-00636801.1 20-SEP-2000; 2000US-00667857; 04-APR-2001; 2001US-00887271.1 18-JUN-2001; 2001US-00884441
                                                                                                                                                                                                                                                                                              Human; immunostimulant; cytostatic; cancer; ovarian
                                                                                                                                                                                                                                                                                                                Ovarian carcinoma antigen polynucleotide
                                                                                                                                                                                                                                                                                                                                      02-JUL-2002
                                                                                                                                                                                                                                                                                                                                                           ABN72602;
                                        Polypeptides comprising an immunogenic portion of an ovar:
protein or its variants, useful for stimulating an immune
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Example 1;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score:
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TTCTGTAGCTGCAGCCACGTGACTGTTGTGGACAGAGCAGTGACCATCACAGACCTTCGA
                PheCysSerCysSerHisValThrValValAspArgAlaValThrIleThrAspLeuArg
                                                                        GluGluIleSerSerCysArgGlnLysGlyPheHisProHisSerLysAspProProLeu
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Search completed: August 23, 2004, 19:20:59 Job time : 559 secs

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Command line parameters:

NODEL-frame+_p2n.model -DEV=xlh
-Q=/cgp2_1/USPTO_Spool/US0931452/runat_17082004_151200_23681/app_query.fasta_1.583
-DB=Issued_Patents_NA -QFMT=fastap_-SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS-human40.cdi
-LIST=45 -DCCALIGN=200 -THR SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=20000000
-USER=US09831452 @CGN_1 1_69 @runat_17082004 151200_23681 -NCPU-6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -MAXIT -DSEBLOCK=100 -LONGLOG
-NMAP -LARGEQUERY -NEG_SCORES=0 -MAXIT -DSEBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -MARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPOEXT=0.5 -FGAPOP=6
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re greater than or equal to the score of the result being printed,
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1: /cgn2_6/ptodata/
2: /cgn2_6/ptodata/
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US-09-665-479A-1
US-09-404-B79A-18
US-09-318-933-18
US-09-215-681-18
US-09-216-003A-18
US-09-216-003A-19
US-09-318-933-19
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Sequence 18, Appl
Sequence 18, Appl
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### ALIGNMENTS

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Sequence 1, Application US/0965479A

Patent NO. 6673570

GENERAL INFORMATION:
APPLICANT: Itch, Funiko
APPLICANT: Itch, Susumu
APPLICANT: Heldin, Carl-Henrik
APPLICANT: ten-Dijke, Peter
TITLE OF INVENTION: SMAD ASSOCIATING POLYPEPTIDES
FILE REFERENCE: L00461.7096.US
CURRENT APPLICATION NUMBER: US/09/665,479A
CURRENT FILING DATE: 2000-9-20
PRIOR APPLICATION NUMBER: US 60/154,846
PRIOR FILING DATE: 1999-09-20
INVESER OF SEQ ID NOS: 20
CONTENER OF SEQ ID NOS: 20
                                  Percent Similarity:
Best Local Similarity:
Query Match:
DB:
US-09-831-452-1 (1-424) x US-09-665-479A-1 (1-2003)
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                                    ThrAlaPheLeuSerSerValAspLeuHisThrHisCysSerTyrGlnMetMetLeuPro
                                                                       CTCATACAGGATCAGCAGGGCCTCATCACACTGGGCTGGATTCATACTCACCCCACACAG
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GENERAL INFORMATION:
APPLICANT: Mincham, Jennifer L.
APPLICANT: Ming, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: DIANNOSIS OF OVARIAN CAN
FILE REFERENCE: 210121.462C2
CURRENT APPLICATION NUMBER: US/09/404,879A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 393
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 18
SEQ ID NO 18
SEQ ID NO 18
CURGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1) T. (1041)
OTHER INFORMATION: n = A,T,C or G
US-09-404-879A-18
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US-09-404-879A-18
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              GluGluIleSerSerCysArgGlnLysGlyPheHisProHisSerLysAspProProLeu
                                                                                                     GlnGlnGlyLeuIleThrLeuGlyTrpIleHisThrHisProThrGlnThrAlaPheLeu
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APPLICANT: Mitcham, Jennifer Lynn
APPLICANT: King, Gordon E.
FILE OF INVENTION: COMPOSITIONS AND METHODS FOR
FILE REFERENCE: 210121.462C1
CURRENT APPLICATION NUMBER: US/09/338,933
CURRENT FILING DATE: 1999-06-23
NUMBER OF SEQ ID NOS: 312
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 18
LENGTH: 1041
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1041)
OTHER INFORMATION: n = A,T,C or G
US-09-338-933-18
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US-09-215-681-18
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Sequence 18, Application Patent No. 6528253 GENERAL INFORMATION: APPLICANT: Mitcham, Jenn
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; SOFTWARE: Pat ; SEQ ID NO 18 ; LENGTH: 1041

PatentIn Ver.

APPLICANT: Mitcham, Jennifer L.
APPLICANT: Frudakis, Tony N.
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS
FILE REFERENCE: 210121.462
CURRENT APPLICATION NUMBER: US/09/216,003A
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 310
SCREWARDS: DATENTO VET 2 0

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THERAPY OF

OVARIAN CANCER

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APPLICANT: Frudakis, Tony N.
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FO
TITLE OF INVENTION: OF OVARIAN CANCER
FILE REFERENCE: 210121.463
CURRENT APPLICATION NUMBER: US/09/215,681A
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 310
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 18
                                              RESULT 5
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Sequence 18, Application US/09216003A Patent No. 6670463
GENERAL INFORMATION:
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NAME/KEY: misc feature
LOCATION: (1)...(1041)
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ORGANISM: Homo sapien
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/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: modified_base
/ LOCATION: (544)
/ OTHER INFORMATION: Where n
US-09-216-003A-18
                                                                                        GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: King, Gordon E.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C2
CURRENT APPLICATION NUMBER: US/09/404,879A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 393
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 19
LENGTH: 1043
TYPE: DNA
ORGANISM: Homo sapien
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ORGANISM: Homo
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Sequence 19, Application US/09338933

Patent NO. 6488931

GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer Lynn
APPLICANT: Mitcham, Jennifer Lynn
APPLICANT: Ming, Gordon E.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FO:
TITLE OF INVENTION: OVARIAN CANCER
FILE REFERENCE: 210121.462C1

CURRENT APPLICATION NUMBER: US/09/338,933

CURRENT FILING DATE: 199-06-23

NUMBER OF SEG ID NOS: 312

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 19
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APPLICANT: Micham, Jennifer L.
APPLICANT: Frudakis, Tony N.
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FO:
ITITLE OF INVENTION: OF OVARIAN CANCER
FILE REFERENCE: 210121.463
CURRENT APPLICATION NUMBER: US/09/215,681A
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 310
SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: FastSEQ for Windows Version 3.0
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; TYPE: DNA
; ORGANISM: Homo sapien
US-09-215-681-19
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                                                   GluGluIleSerSerCysArgGlnLysGlyPheHisProHisSerLysAspProProLeu
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   PheCysSerCysSerHisValThrValValAspArgAlaValThrIleThrAspLeuArg
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US-09-651-011A-3
US-09-651-011A-3
Sequence 3, Application US/09651011A
Sequence 3, Application US/09651011A
Sequence 3, Application US/09651011A
GENERAL INFORMATION:
APPLICANT: Nicholas M. Dean
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF HPK/GCK-LIKE
FILE REFERENCE: RTS-0168
CURRENT APPLICATION NUMBER: US/09/651,011A
CURRENT FILING DATE: 2000-08-29
NUMBER OF SEQ ID NOS: 49
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APPLICANT: Micham, Jennifer L.
APPLICANT: Fridakis, Tony N.
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
FILE REFERENCE: 210121.462
CURRENT APPLICATION NUMBER: US/09/216,003A
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 310
SOCTWARE: Patentin Ver. 2.0
SEQ ID NO 10 A0 3
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TYPE: DNA
ORGANISM: Homo sapiens
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TYPE: DNA
ORGANISM: Homo
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                                                CCACCAGTGCCTTCCCGATCA---GAGTCTTTTTCCAATGGCAACTCCGAGTCTGTGCAT 1632
                                                                          ProProValValAspArgSerLeuLysProGlyAlaLeuSerAspSerGluSer-----
                                                                                                     AAAACTAACCACAGCTCCCCTGAA----GCCCAGTCTAAGCAGACAGGCAGAGTATTGGAG
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CURRENT APPLICATION DATA;
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FILING DATE: 18-SEP-1989
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                             GluLysGluLysGlnArgValAlaGlnGlnLysGlnGlnGlnLeuGluGlnGluGlnPhe 162
                                                                                             LysLysGluAlaGluGluLeuAla------ArgAsnMetAlaIleGlnGlnGluLeu 142
                                                                                                                              GAGGTTGAAGAATTCTACCAGAAGAAGATAAA-----AATGAAAAAGGTCAACATGAA 1668
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US-09-566-921-42
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APPLICANT: Tingley, Debora W.
APPLICANT: Edwards, Carla W.
APPLICANT: Edwards, Carla W.
TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE
FILE REFERENCE: PA-0024 US
CURRENT FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 138
SOFTWARE: PERL Program
SEQ ID NO 42
**TYPONT***
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No
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3650 GAAGACATTCCATCAAGGACAGAGGAACCAAGT---GAGAAGAAGGTACCTCTGGACATG 3706
                                                                                                                                         3530 GACCTCAAGGAAGAGATGACCCTTATGGTGCATGTGCCTAAGCCTGGACACAAGAGAAACA
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                                   89 LysAspThrValLysLysLeuLysGluIleAlaPheProLysAlaGluGluLeuLysAla
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                                                                                                                                                                                                                                                 42 GluileIleArgMetAlaSerIleTyrSerGluGluGlyAsnIleGluHisAlaPheIle
                                                                       GACTCCACCCACAGCAGCAACGAGTCTGAATATATCTTTAGCTCTGAAATTGCAGAAATG
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                                             APPLICANT: PLOWMAN, GREGORY
APPLICANT: MARTINEZ, RICARDO
APPLICANT: WHYTE, DAVID
ITILE OF INVENTION: STE20-RELATED PROTEIN KINASES
FILE REFERENCE: 038602/0328
CURRENT APPLICATION NUMBER: US/09/688,188B
CURRENT FILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: 09/291,417
PRIOR APPLICATION NUMBER: 09/291,417
PRIOR APPLICATION NUMBER: 09/291,417
PRIOR FILING DATE: 1999-04-14
PRIOR FILING DATE: 1998-04-14
PRIOR FILING DATE: 1998-04-14
NUMBER OF SEQ. ID NOS: 155
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US-09-688-188B-9
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               SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 9
                                                                                                                                                                                                                                                                                   Sequence 9, Application US/09688188B Patent No. 6656716
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 LENGTH: 3798
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                                                                                                                                                                                                                                                                                                                                                                                                                                              AGATCATCTGCTCTGGATTACCATGAGTTGAATGAGGATGGAGAG
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; ORGANISM: Homo
US-09-688-188B-9
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                                                                                                                                                                                                                                                                                                                                                                                                            TATATCAGGCGACAGCTAGAAGAGGAGCAGCGGCAC----
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                               MetArgAsnGluPheThrIleThrHisValLeuIleProLysGlnSerAlaGlySerAsp 309
                                                                                        LeuAlaSerAlaAsnThrAlaArgGlyValGluThrCysGlyIleLeuCysGlyLysLeu
                                                                                                                                             ThrlleAspGlyLeuArgHisValValValProGlyArgLeuCysProGlnPheLeuGln
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APPLICANT: PLOWMAN, GREGORY
APPLICANT: WARTINEZ, RICARDO
APPLICANT: WAYTE, DAVID
FILE REFERENCE: 038602/0329
CURRENT APPLICATION: STE20-RELATED PROTEIN KINASES
FILE REFERENCE: 038602/0329
CURRENT ILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: 05/09/291,417D
CURRENT FILING DATE: 1998-04-14
NUMBER OF SEQ ID NOS: 155
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 9
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US-09-291-417D-9
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                         TyrLysSerAlaValIleProGluLysLysAspThrValLysLysLeuLysGlu-----
                                                                                                                    GGTGAGTCTACTCTTCGCCGAGATTTCCTGAGACTGCAGCAGGAGAACAAGGAACGTTCC
                                                                                                                                                 GlyValGluIleIleArgMetAlaSerIleTyrSerGluGluGlyAsnIleGluHisAla 59
                                                                                                                                                                               GAAGAAGAGGAAGTGCCTGAACAGGAAGGAGGCCAAGTTCCATTGTGAACGTGCCT 1047
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Gaps:
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RESULT 15
US-09-645-456A-6
; Sequence 6, Application
; Patent No. 6562580
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                 SerPro-----LysPheGlnGluThrGlyPhePheLysLeuThrAspHisGlyLeuGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                             GATTTAGGAAAACTAACCACAGCTCCCCTGAAGCCCAGTCTAAGCAGACAGGCAGAGTAT 1780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ThrLeuGlyTrpIleHisThrHisProThrGlnThrAlaPheLeuSerSerValAspLeu
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TITLE OF INVENTION: METHODS OF USE

FILE REFERENCE: A-68344/EMS/DHR
CURRENT FILING DATE: 2000-08-24

PRIOR APPLICATION NUMBER: US/09/645,456A

CURRENT FILING DATE: 2000-08-24

PRIOR APPLICATION NUMBER: US/09/425,324

PRIOR FILING DATE: 1999-10-21

NUMBER: OF SEQ ID NOS: 36

SOFTWARE: Patentin version 3.1

LENGTH: 3972
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OTHER INFORMATION: synthetic
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CGGCAGGAGCAGAGGCTGTGGAGAAGAAGCCACTGTACCATTACAAAGAAGGAATGAGT
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GAAAGACTGCAGAGGCTAAGCTAAGCAAGAAAGAGACTACTTAGTTTCCCCTTCAGCATCAG
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                                       ACCGCCTCCCAGTCAGTGCACGAGCAGCCCACA
                                                                                                                         CCAGTCGATCCCCAGATCCCACATCTGGTAGCTGTAAAAATCCCAGGGACCT----GCCTTG 172
                                                                                                                                                                                                                                               ---PheProThrLeuThrValSerSerIleGlnProSerAspCysHisThrThrValArg 226
                                                                                                                                                                                                                                                                                           AGTTCCCCTGCCATGCCTCACAAGGTTGCCAACAGGATATCTGACCCCAACCTGCCCCCA
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Search completed: August 23, 2004, 21:49:49 Job time : 120 secs

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Maximum Match 100%
Listing first 45 summaries
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   US-10-784-004-756
US-10-784-004-1100
US-10-170-205E-30458
US-10-170-205E-30459
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US-10-784-004-954
US-10-784-004-954
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US-10-425-115-311198
US-10-767-701-41925
US-10-820-583A-6618
US-10-767-701-40123
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Sequence 756, App
Sequence 1100, Ap
Sequence 31035, A
Sequence 31635, A
Sequence 439, App
Sequence 116, App
Sequence 21521, A
Sequence 21521, A
Sequence 1185, A
Sequence 19859, A
Sequence 6515, A
Sequence 511201,
Sequence 511201,
Sequence 511201,
Sequence 615, App
Sequence 615, App
Sequence 41925, A
Sequence 6115, Ap
Sequence 41925, A
Sequence 41925, A
Sequence 41921, Ap
Sequence 41131, Ap
Sequence 1512, Ap
Sequence 40123, A
Sequence 4181, Ap
Sequence 4181, Ap
Sequence 4181, Ap
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GENERAL INFORMATION:
APPLICANT: Blogen Idec
ITILE OF INVENTION: Surrogate Markers of Pain
FILE REFERENCE: 08201.6029-00000
CURRENT APPLICATION NUMBER: US/10/784,004
CURRENT FILING DATE: 2004-02-20
NUMBER OF SEQ ID NOS: 1251
SOFTWARE: PatentIn version 3.2
SEQ ID NO 756
LENGTH: 424
TYPE: PRT
GROANISM: human
US-10-784-004-756
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Best Local Similarity 100.0%;
Matches 424; Conservative 0;
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Sequence 2	Sequence 8:	Sequence 2	Sequence 2	Sequence 1	Sequence 6	Sequence 2	Sequence 6	Sequence 6	Sequence 4	Sequence 8	Sequence 8	Sequence 3.	Sequence 2	Sequence 2	Sequence 2	Sequence 1	Sequence 1	Sequence 1
20582, A	8238, Ap	27197, A	26, Appl	1510, Ap	6619, Ap	22882, A	610, App	610, App	4, Appli	89, Appl	9, Appl	336996,	22664, A	240, App	241, App	18080, A	1735, Ap	19618, A

### ALIGNMENTS

Дb	γQ	Дb	82	DЬ	80	В	Qy	DЬ	Qy	DЬ	8	Дb	8	Matches	Query
361 ESVAIVCSPKFQETGFFKLTDHGLEEISSCRQKGFHPHSKDPPLFCSCSHVTVVDRAVTI 420	361 ESVAIVCSPKFQETGFFKLTDHGLEEISSCRQKGFHPHSKDPPLFCSCSHVTVVDRAVTI 420	301 IPKQSAGSDYCNTENBEELFLIQDQQGLITLGWIHTHPTQTAFLSSVDLHTHCSYQMMLP 360	301 IPKQSAGSDYCNTENEEELFLIQDQQGLITLGWIHTHPTQTAFLSSVDLHTHCSYQMMLP 360	241 ALSNSESIPTIDGLKHVVVPGKLCPQFLQLASANTARGVETCGILCGKLMRNEFTITHVL 300	241 ALSNSESIPTIDGLRHVVVPGRLCPQFLQLASANTARGVETCGILCGKLMRNEFTITHVL 300	181 IVQEFGKVDPGLGGELVPDLEKPSLDVPPTLTVSSIQPSDCHTTVRPAKPPVVDRSLKPG 240	181 IVQEFGKVDPGLGGPLVPDLEKPSLDVFPTLTVSSIQPSDCHTTVRPAKPPVVDRSLKPG 240	121 YNEEKKKEAEELARNMAIQQELEKEKQRVAQQKQQQLEQEQFHAFEEMIRNQELEKERLK 180	121 YNESKKKBAEELARNMAIQQELEKEKQRVAQQKQQQLEQEQFHAFEEMIRNQELEKERLK 180	61 ILYNKYITLFIEKLPXHRDYKSAVIPEKKDTVKKLKEIAFPKAEELLKRYTKEYTE 120	61 ILYNKYITLFIEKLPXHRDYKSAVIPEKKDTVKKLKEIAFPKAEELKAELLKRYTKEYTE 120	1 MSDHGDVSLPPEDRVRALSQLGSAVEVNEDIPPRRYFRSGVEIIRMASIYSEEGNIEHAF 60	1 MSDHGDVSLPPEDRVRALSQLGSAVEVNEDIPPRRYFRSGVEIIRMASIYSEEGNIEHAF 60	424; Conservative 0; Mismatche	Query Match 100.0%; Score 2208; DB 6; Length 424;

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Sequence 30458, Application US/10170205E

GENERAL INFORMATION:
APPLICANT: ADAMS, Mark

TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COME
TITLE OF INVENTION: CAPTURE AGENTS, AND USES THE
FILE REFERENCE: CL001381
CURRENT APPLICATION UNMBER: US/10/170,205E
CURRENT FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 40312
SOFTWARE: Patentin version 3.2
SEQ ID NO 30458
LENGTH: 424
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(GENERAL INFORMATION:
APPLICANT: Biggen Idec
TITLE OF INVENTION: Surrogate Markers of Pair FILE REFERENCE: 08201.6029-00000
CURRENT APPLICATION UNMBER: US/10/784,004
CURRENT FILING DATE: 2004-02-20
UNMBER OF SEQ ID NOS: 1251
SOFTWARE: Patentin version 3.2
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US-10-170-205E-30458
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Pred. No. 1.3e-146;
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US-10-170-205E-31635
US-10-170-205E-31635
Sequence 31635, Application US/10170205E
GENERAL INFORMATION:
APPLICANT: ADAMS, Mark
TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMFITILE OF INVENTION: CAPTURE AGENTS, AND USES THE FILE REFERENCE: CL00131
CURRENT APPLICATION NUMBER: US/10/170,205E
CURRENT FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 40312
SOFTWARE: PatentIn version 3.2
LENGTH: 424
THE OF SEQ ID NO 31635
LENGTH: 424
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US-10-170-205E-31635
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Best Local Similarity
Matches 424; Conserv
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YNEEKKKEAEELARNMAIQOELEKEKQRVAQQKQQLEQEQFHAFEEMIRNQELEKERLK
                                                             | ILYNKYITLFIEKLPKHRDYKSAVIPEKKDTVKKLKBIAFPKAEELKAELLKRYTKEYTE 120
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Pred. No. 1.3e-146;
D; Mismatches 0;
                                                                                                                                                                                                                                              Score 2208; DB 6;
Pred. No. 1.3e-146;
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Sequence 30459; Application US/10170205E
; GENERAL INFORMATION:
; APPLICANT: ADAMS, Mark
; TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMP
; TITLE OF INVENTION: CAPTURE AGENTS, AND USES THE
; FILE REFERENCE: CL001381
; CURRENT APPLICATION NUMBER: US/10/170,205E
; CURRENT FILING DATE: 2002-06-13
; NUMBER OF SEQ 'ID NOS: 40312
; SOFTMARE: PatentIn version 3.2
; SEQ ID NO 30459
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-170-205E-30459
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US-10-170-205E-30459
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Best Local Similarity
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GENERAL INFORMATION:
APPLICANT: Biogen Idec
TITLE OF INVENTION: Surrogate Markers of Pain
FILE REFERENCE: 08201.6029-00000
CURRENT APPLICATION NUMBER: US/10/784,004
CURRENT FILING DATE: 2004-02-20
NUMBER OF SEQ ID NOS: 1251
SOFTWARE: Patentin version 3.2
SEG ID NO 439
                                   ; LENGTH: 424
; TYPE: PRT
; ORGANISM: rat
US-10-784-004-954
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US-10-784-004-439
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                                                                                                 NUMBER OF SEQ ID NOS: 1251
SOFTWARE: PatentIn version 3.2
SEQ ID NO 954
                                                                                                                                                            Sequence 954, Application US/10784004
GENERAL INFORMATION:
APPLICANY: Biogen Idec
TITLE OF INVENTION: Surrogate Markers of 1
FILE REFERENCE: 08201.6029-00000
CURRENT APPLICATION NUMBER: US/10/784,004
CURRENT FILING DATE: 2004-02-20
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Best Local Simi
Matches 357;
Query Match
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TYPE: PRT
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Pred. No. 5.5e-126;
3; Mismatches 34;
 Score 1913;
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Length 424;
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Matches

357;

Conservative

84.2%; 33;

Pred. No. 5.5e-126; Mismatches

34;

Indels

0

Best Local Similarity

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APPLICANT: WU,THOMAS D.
TITLE OF INVENTION: Compositions and Methods fo:
TITLE OF INVENTION: Related Diseases
FILE REFERENCE: P1948R1-US
CURRENT APPLICATION NUMBER: US/10/370,715B
CURRENT FILING DATE: 2003-02-21
NUMBER OF SEQ ID NOS: 742
SEQ ID NO 116
LENGTH: 463
TYPE: PRT
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US-10-370-715B-116
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                                                                                                                                 Query Match
Best Local !
                                                                                                                     Matches
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APPLICANT: BOARY, SARAH C.
APPLICANT: CLARK, HILLARY
APPLICANT: BRISDELL, HUNNTE
APPLICANT: BRISDELL, JANET
                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                         ORGANISM: Homo sapien
                                                                                                                  Match 55.7%; Score 1229.5; DB 6; Local Similarity 56.4%; Pred. No. 4.2e-78; es 232; Conservative 72; Mismatches 92;
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                    ILYNKYITLFIEKLPKHRDYKSAVIPEKKDTVKKLKEIAFPKAEELKAELLKRYTKEYTE
                                                          MPDHTDVSLSPEERVRALSKLGCNITISEDITPRRYFRSGVEMERMASVYLEEGNLENAF
                                                                           MSDHGDVSLPPEDRVRALSQLGSAVEVNEDIPPRRYFRSGVEIIRMASIYSEEGNIEHAF
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   VLYNKFITLFVEKLPNHRDYQQCAVPEKQDIMKKLKEIAFPRTDELKNDLLKKYNVEYQE
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JACKMAN, JANET
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US-10-170-205E-21521

JS-10-170-205E-21521

Sequence 21521, Application US/10170205E

GENERAL INFORMATION:

APPLICANT: ADAMS, Mark

TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMI

TITLE OF INVENTION: CAPTURE AGENTS, AND USES THE

CURRENT APPLICATION NUMBER: US/10/170,205E

CURRENT ETLING DATE: 2002-06-13

NUMBER OF SEQ ID NOS: 40312

SEQ ID NO 21521

LENGTH: 463

TURNEL DEVICE: 1001

LENGTH: 463
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Best Local
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YQLMLPEAIAIVCSPKHXDTGIFRLTNAGMLEVSACKKKGFHPHTKEPRLF
                                                                TITHVIVPKQSAGPDYCDMENVEELFNVQDQHDLLTLGWIHTHPTQTAFLSSVDLHTHCS
                                                                                    TITHVLIPKQSAGSDYCNTENEEELFLIQDQQGLITLGWIHTHPTQTAFLSSVDLHTHCS
                                                                                                                                                                                                                          IVOEFGKVDPGLGGPLVPDLEKPSLDVFPT-----LTVSSIQPSDCHTTVRPAKPPVVD 234
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                       YQMMLPESVAIVCSPKFQETGFFKLTDHGLEEISSCRQKGFHPHSKDPPLF
                                                                                                                             RALTPAATLSAVQNLVVEGLRCVVLPEDLCHKFLQLAESNTVRGIETCGILCGKLTHNEF
                                                                                                                                                          RSIKPGALSNSESIFTIDGLRHVVVPGRICPQFIQLASANTARGVETCGILGGKLMRNEF 294
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Pred. No. 4.2e-78;
2; Mismatches 92;
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RESULT 11
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Sequence 311202, Application US/10425115
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 45299
LENGTH: 507
TYPE: PRT
ORGANISM: Sorghum bicolor
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Best Local
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APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535) B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
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NAME/KEY: unsure
LOCATION: (1)..(507)
OTHER INFORMATION: unsure
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                                                                                                                                                                                                  RGFHPH-KAPLDGSPIYEQCSHVYMDNDIKFDMIDLR
                                                                                                                                                                                                                                        KGFHPHSKDP----PLFCSCSHVTV-VDRAVTITDLR 424
                                                                                                                                                                                                                                                                                                              THETOTAFLSSVDLHTHCSYQMMLPESVAIVCSP--KFQETGFFKLTD-HGLEEISSCRQ
                                                                                                                                                                                                                                                                                                                                                       KRSLETCGVLAGTLKKRTFCVTTLIIPKQKSTSNTCEAINEEELFEVQDTGSLFTLGWIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SVOKOFMNLPYPKEETLARHSILGPNGLNGRWNGPVTEIKVOYPSNFELSTRDITSLVPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ITLFIEKLPKHRDYKSAVIPEKKDTVKKLKEIA-FPKAEELKAEL--LKRYT-KEYTEYN
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                                                                                                                                                                                                                                                                                                                                                                                             ARGVETCGILCGKLMRNEFTITHVLIPKQSAGSDYCNTENEEELFLIQDQQGLITLGWIH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSLLCETIPKHRDYHAF-----KLKEKAFFDKLNDVMKELETLKPVVQRQVAEHN
                                                                                                                                                                                                                                                                             THPTQSCXLSSIDLHNHYSYQVMLPEAIAIVMAPIDTTRKHGIFHLTDPGGMGVIHDCQE
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ORGANISM: Zea mays

Other Molecules

Associated With

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US-10-425-115-198593

US-10-425-115-198593

Sequence 198593, Application US/10425115

GENERAL INFORMATION:

APPLICANT: LA ROSA, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Oth

TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21(53222)B

CURRENT APPLICATION UNMBER: US/10/425,115

CURRENT APPLICATION UNMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 198593

LENGTH: 408

TYPE: PRT
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US-10-425-115-311202
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Best Local
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ORGANISM: Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 IAVDHRISLPYYFRIAGSLLRQANIYRNESNFLDLYVILLRYSSLLCETIPRHRDYHAFK 80
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30.3%; Pre-
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Pred. No. 1.6e-28;
3; Mismatches 162;
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US-10-767-701-40264
                                                                                                                                                                                                                        TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement FILE REFERENCE: 38-21 (53535) B CURRENT APPLICATION NUMBER: US/10/767,701 CURRENT FILING DATE: 2004-01-29 NUMBER OF SEQ ID NOS: 63128 SEQ ID NO 40264 LENGTH: 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 137; Conserv
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                                                                      Matches
                                                                                                       Query Match
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APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(408)
OTHER INFORMATION: unsure at all Xaa locations
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                                                                                                                                                                                           ORGANISM: Sorghum bicolor
                                                                                                                                                                           FEATURE:
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                                                                      l Similarity
87; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SILGPNGLQWYRDGFSSHXRHDHVXRLKNLXTPVALMECFLRLAEXNTXKNLEXCGILAG
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                                    PPVVDRSLKPGALSNSESIPTIDGLRHVVVPGRLCPQFLQLASANTARGVETCGILCGKL 289
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       Conservative
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                                                                        18.6%; Score 411.5; DB 6
46.3%; Pred. No. 2.6e-21;
tive 31; Mismatches 59
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Pred. No. 4.5e-28;
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Sequence 6915, Application US/10793479

GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Uscelert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Enc.
FILE REFERENCE: 59.052.REG
CURRENT APPLICATION NUMBER: US/10/793,479

CURRENT FILING DATE: 2004-03-03

PRIOR APPLICATION NUMBER: US/09/513,999

PRIOR APPLICATION NUMBER: US/09/513,999

PRIOR APPLICATION NUMBER: US/09/513,999

PRIOR APPLICATION NUMBER: US/09/513,999

PRIOR FILING DATE: 1999-02-26

PRIOR FILING DATE: 1999-02-26

PRIOR FILING DATE: 1999-02-26

PRIOR FILING DATE: 1999-02-26
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US-10-425-115-311201
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US-10-793-479-6915
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APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT TILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 311201
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FLRVAESNTKRSLETCGVLAGTLKNRTFYVTTLIIPKQKSTSVTCEATNEEELFEVQDMG 65
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Pred. No. 1.6e-20;
3; Mismatches 46
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                                                                                                                                                                               Encoded Human Proteins
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SOFTWARE: Patent.pm

SEQ ID NO 6915

LENGTH: 78

TYPE: PRT

ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: UNSURE
LOCATION: 31

OTHER INFORMATION: Xaa=Flo or Arg

UNCATION: 33

OTHER INFORMATION: Xaa=Pro or Arg

US-10-793-479-6915

Query Matches 76; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Matches 76; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Matches 76; Conservative 0; Mismatches 0; Gaps 0;

Matches 76; Conservative 0; Mismatches 0; Gaps 0;

OTHER INFORMATION: Xaa=Pro or Arg

OFFICIAL Similarity 97.4%; Pred. No. 4e-20;
Matches 76; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Matches 76; Conservative 0; Mismatches 0; Gaps 0;

ORGANISM: Argument of the conservation of
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Database :
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Maximum DB seq
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length: 2000000000
               August 17, 2004, 14:57:49; Search time 177 Seconds (without alignments) 2338.117 Million cell updates/sec
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Gapop 10.0 , Gapext 0.5
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Maximum Match 100%
Listing first 45 summaries
/ Cgn2_6/ptodata/2/paa/US08_COMB.pep: *
/ Cgn2_6/ptodata/2/paa/US08_COMB.pep: *
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/ Cgn2_6/ptodata/2/paa/US082_COMB.pep: *
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/ Cgn2_6/ptodata/2/paa/US082_COMB.pep: *
/ Cgn2_6/ptodata/2/paa/US085_COMB.pep: *
/ Cgn2_6/ptodata/2/paa/US095_COMB.pep: *
/ Cgn2_6/ptodata/2/paa/US090_COMB.pep: *
/ Cgn2_6/ptodata/2/paa/US090_COMB.pep: *
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/ Cgn2_6/ptodata/2/paa/US095_COMB.pep: *
/ Cgn2_6/ptodata/2/paa/US095_COMB.pep: *
/ Cgn2_6/ptodata/2/paa/US096_COMB.pep: *
/ Cgn2_6/ptodata/2/paa/US100_COMB.pep: *
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cgn2_6/ptodata/2/paa/US06_0
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equence 2534,	equence 2484,	e 309	equence 3090,	equence 3090,	equence 16473	equence 167,	equence 68,	equence 3556,	equence 3556, A	equence 6, Appl	equence 6, App	equence 3556, A	quence 6, Appli	equence 67, App		equence 5, Appl	quence 5, Appli	equence 3, Appl	equence 3, Appl	equence 15018,	equence 8194, A	equence 8194, A	equence 15018,	equence 15018,	equence 24061,	equence 15017,	equence 15016,	equence 8193, F	equence 8192, 1	equence 8193, A	equence 8192. I	equence 15017.	equence 15016.	emience 15017	equence 15016.	equence 24060.	equence 24059.	equence 2, App.	equence 1, App	equence 66, App	equence 7, App.	quence 7,	equence 1, App	Ď

## ALIGNMENTS

RESULT 1 PCT-US02-00976-7

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Sequence 7. Application PC/TUS0200976
GENERAL INFORMATION:
APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY
APPLICANT: COPE, Gregory
APPLICANT: COPE, Gregory
APPLICANT: VERMA, Rati
APPLICANT: VERMA, Rati
APPLICANT: KOONIN, L.
APPLICANT: KOONIN, Eugene V.
APPLICANT: KOONIN, Eugene V.
APPLICANT: DESHAIES, Raymond
TITLE OF INVENTION FEGULATION OF TARGET PROTEIN ACTIVITY THROUGH MODIFIER PROTEINS
FILE REFERENCE: CIT1510-4W0
CURRENT APPLICATION NUMBER: PCT/US02/00976
CURRENT APPLICATION NUMBER: US 60/22/314
PRIOR APPLICATION NUMBER: US 60/261,314
PRIOR APPLICATION NUMBER: US 60/322,322
PRIOR APPLICATION NUMBER: US 60/322,322
PRIOR FILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: US 60/322,322
PRIOR FILING DATE: 2001-09-14
PRIOR FILING DATE: 2001-09-14
PRIOR FILING DATE: 2001-09-14
SOFTWARE: Patentin version 3.1
SEQ ID NO 7
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Result No.

Score

Query Match Length DB

IJ

Description

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Sequence 1, Application US/09831452

Sequence 1, Application US/09831452

; APPLICANT: SUGAMURA, Kazuo

; APPLICANT: TANAKA, Nobuyuki

TITLE OF INVENTION: Protein AMSH and cDNA thereof

FILE REFERENCE: 2001-0572A/LC/00653

CURRENT APPLICATION NUMBER: US/09/831,452

CURRENT FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: PCT/JP99/06309

PRIOR FILING DATE: 1999-11-12

PRIOR FILING DATE: 1998-11-12

PRIOR FILING DATE: 1998-11-12

PRIOR FILING DATE: 1998-11-12

ONUMBER OF SEQ ID NOS: 4

SOFTMARE: Patentin Ver. 2.0

SEQ ID NO 1

LENGTH: 424

TYPE: PAT

ORGANISM: Homo sapiens
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ILYNKYITLFIEKLPKHRDYKSAVIPEKKDTVKKLKEIAFPKAEELKAELLKRYTKEYTE
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                                                                                             Score 2208; DB 23;
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OS-10-0-8-901.

Sequence 7, Application US/10046961

Sequence 7, Application US/10046961

APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY

APPLICANT: VERMA, Rati
APPLICANT: VERMA, Rati
APPLICANT: DESHAIES, Raymond

APPLICANT: DESHAIES, Raymond

FILE REFERENCE: CIT1510-3

CURRENT APPLICATION NUMBER: US/10/046,961

CURRENT APPLICATION NUMBER: US 60/261,314

PRIOR APPLICATION NUMBER: US 60/261,314

PRIOR APPLICATION NUMBER: US 60/322,322

PRIOR FILING DATE: 2001-09-14

PRIOR APPLICATION NUMBER: US 60/322,322

PRIOR APPLICATION NUMBER: US 60/322,030

PRIOR FILING DATE: 2001-09-14

NUMBER OF SEQ ID NOS: 22

SOFTWARE: PatentIn version 3.1

LENGTH A24
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TYPE: PRT
ORGANISM: Homo sapiens
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                   IVQEFGKVDPGLGGPLVPDLEKPSLDVFPTLIVSSIQPSDCHTTVRPAKPPVVDRSLKPG
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RESULT 4

US-10-047-253-7

US-10-047-253-7

Sequence 7, Application US/10047253

Sequence 7, Application US/10047253

GENERAL INFORMATION:

APPLICANT: COPE, Gregory

APPLICANT: COPE, Gregory

APPLICANT: WERMA, Rati

APPLICANT: WERMA, Rati

APPLICANT: KOONIN, L

APPLICANT: WOUND, ENGUNATION OF TARGET PROTEIN ACTIVITY THROUGH MODIFIER PROTEINS

FILE REFERENCE: CT1510-4

CURRENT APPLICATION NUMBER: US/10/047,253

CURRENT APPLICATION NUMBER: US/0/047,253

CURRENT FILING DATE: 2001-01-12

PRIOR APPLICATION NUMBER: US 60/261,314

PRIOR APPLICATION NUMBER: US 60/322,322

PRIOR APPLICATION NUMBER: US 60/322,322

PRIOR FILING DATE: 2001-09-14

NUMBER: OF SEQ ID NOS: 22

SOFTWARE: Patentin version 3.1

SEQ ID NO 7

LENGTH: 424

TYPE: PRT

ORGANISM: Homo sapiens
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    IPKQSAGSDYCNTENEEELFLIQDQQGLITLGWIHTHPTQTAFLSSVDLHTHCSYQMMLP
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US-10-340-578-66
Sequence 66, Application US/10340578
GENERAL INFORMATION:
APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY
APPLICANT: DESHARES, Raymond J.
APPLICANT: DESHARES, Raymond J.
APPLICANT: VERMA, Rati
APPLICANT: VERMA, Rati
APPLICANT: NARROGGIO, Xavier I.
TITLE OF INVENTION: MODULATION OF COP9 SIGNALSOME ISOPEPTIDASE ACTIVITY
FILLE REFERENCE: CIT1590-1
CURRENT APPLICATION NUMBER: US/10/340.578
CURRENT APPLICATION NUMBER: US 60/355,334
PRIOR APPLICATION NUMBER: US 10/047,253
PRIOR APPLICATION NUMBER: US 10/047,253
PRIOR FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: US 10/046,961
PRIOR APPLICATION NUMBER: US 60/261,314
PRIOR APPLICATION NUMBER: US 60/261,314
PRIOR APPLICATION NUMBER: US 60/362,322
PRIOR APPLICATION NUMBER: US 60/322,322
PRIOR FILING DATE: 2001-09-14
PRIOR FILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: US 60/322,322
PRIOR FILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: US 60/322,320
PRIOR FILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: US 60/322,330
PRIOR FILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: US 60/322,330
PRIOR FILING DATE: 2001-09-14
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ESVAIVCSPKFQETGFFKLTDHGLEEISSCRQKGFHPHSKDPPLFCSCSHVTVVDRAVTI
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Sequence 1, Application US/10671572A
GENERAL INFORMATION:
APPLICANT: SIGMAURA, Kazuo
APPLICANT: TANAKA, Nobuyuki
TITLE OF INVENTION: Protein AMSH and cDNA thereof
FILL REFERENCE: 2003-1382/WMC/00653
CURRENT APPLICATION NUMBER: US/10/671,572A
CURRENT FILING DATE: 2003-09-29
PRIOR APPLICATION NUMBER: 09/831,452
PRIOR APPLICATION NUMBER: POT/JP99/06309
PRIOR APPLICATION NUMBER: POT/JP99/06309
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: US NO. 10-322674
PRIOR FILING DATE: 1998-11-12
SOFTWARE: PATENTING DATE: 1998-11-12
NUMBER OF SEQ ID NOS: 4
PRIOR FILING DATE: 1998-11-12
SOFTWARE: PATENTING DATE: 1998-11-12
SOFTWARE: PATENTING DATE: 1998-11-12
SOFTWARE: PATENTING DATE: 1998-11-12
RESULT 7
US-10-752-442-2
; Sequence 2, Application US/10752442
; GENERAL INFORMATION:
() APPLICANT: Itoh, Fumiko
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US-10-671-572A-1
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Best Local
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TYPE: PRT
ORGANISM: Homo sapiens
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Pred. No. 3.1e-172;
Mismatches 0;
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      ORGANISM: Homo sapiens
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APPLICANT: Itoh, Susumu
APPLICANT: Heldin, Carl-Henrik
APPLICANT: Heldin, Carl-Henrik
TITLE OF INVENTION: SWAD ASSOCIATING POLYPEPTIDES
FILE REFERENCE: L0461,70096US01
CURRENT APPLICATION NUMBER: US/10/752,442
CURRENT FILING DATE: 2004-01-06
PRIOR APPLICATION NUMBER: US 09/665,479
PRIOR FILING DATE: 2000-09-20
PRIOR FILING DATE: 1909-09-20
PRIOR FILING DATE: 1999-09-20
NUMBER OF SEQ ID NOS: 20
SOCTWARE: Patentin version 3.2
SEQ ID NO 2
TENGTH: 424
APPLICANT: CARGILL, Michele
APPLICANT: GRUPE, Andrew
TITLE OF INVENTION: GENETIC POLYMORPHISMS AS:
TITLE OF INVENTION: ALLHEIMER'S DISEASE, ME:
FILE REFERENCE: CL001450
CURRENT APPLICATION NUMBER: US/60/452,680
CURRENT FILING DATE: 2003-03-07
NUMBER OF SEQ ID NOS: 116213
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 24059
LENGTH: 424
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; TYPE: PRT
; ORGANISM: Homo s
US-10-752-442-2
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US-60-452-680-24059
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Matches 424; Conserv
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Pred. No. 3.1e-172;
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RESULT 9
US-60-452-680-24060
; Sequence 24060, Application US/60452680
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                   APPLICANT: CARGILL, Michele
APPLICANT: GRUPE, Andrew
TITLE OF INVENTION: GRUPET POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1450
CURRENT APPLICATION UNMEER: US/60/452,680
CURRENT FILING DATE: 2003-03-07
NUMBER OF SEQ ID NOS: 116213
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 24660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 424; Conservative
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TYPE: PRT
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                                                                                                                                       Score 2208; DB 33;
Pred. No. 3.1e-172;
; Mismatches 0;
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Pred. No. 3.1e-172;
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US-60-453-050-15016
/ Sequence 15016, Application US/60453050
/ GENERAL INFORMATION:
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APPLICANT: LIKE, Michele

APPLICANT: LUKE, May

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001457

CURRENT APPLICATION NUMBER: US/60/453,050

CURRENT FILING DATE: 2003-03-10

NUMBER OF SEQ ID NOS: 82762

SOOTMARE: FRASESEQ for Windows Version 4.0

EENGTH: 424

TYPE: PAT

ORGANISM: Homo sapiens

US-60-453-050-15016
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TDLR 424

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RESULT 12
US-60-453-135-15016
; Sequence 15016, Application US/60453135
; GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
; APPLICANT: CARGILL, Michele
; APPLICANT: CARGILL, Michele
; APPLICANT: CARGILL, MICHEL
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DET
; FILE REFERENCE: CL001456
; CURRENT APPLICATION UNMBER: US/60/453,135
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 82762
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: LIKE, May

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF

FILE REPERBENCE: CL001457

CURRENT APPLICATION NUMBER: US/60/453,050

CURRENT APPLICATION NUMBER: US/60/453,050

NUMBER OF SEQ ID NOS: 82762

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 15017
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TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLORATION UNMBER: US/60/453,135
CURRENT APPLICATION UNMBER: US/60/453,135
CURRENT FILING DATE: 2003-03-10
INUMBER: OF SEQ ID NOS: 82762
SOOTWAREN: FRASTSEQ for Windows Version 4.0
SEQ ID NO 15017
LENGTH: 424
TYPE: bor
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US-60-453-135-15017

Sequence 15017, Application US/60453135

GENERAL INFORMATION:
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SEQ ID NO 15016
LENGTH: 424
TYPE: PRT
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Best Local
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Pred. No. 3.1e-172;
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Pred. No. 3.1e-172;
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US-60-455-444-8192
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michale
APPLICANT: BEGOVICH, Ann
ITILE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: HEIGMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001455
FILE REFERENCE: CL001455
CURRENT APPLICATION NUMBER: US/60/455,444
CURRENT FILING DATE: 2003-03-18
RUMBER OF SEQ ID NOS: 50986
SOFTWARE: FASTSEQ for Windows Version 4.0
LENGTH: 424
TYPE: DETECTION REPORTS OF THE PROPERTY OF THE PROPER
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Pred. No. 3.1e-172;
; Mismatches 0;
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RESULT 15

US-60-455-444-8193

JS-60-455-444-8193

Sequence 8193, Application US/60455444

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele

APPLICANT: BECOVICH, Ann

TITLE OF INVENTION: GENETIC POLYMORPHISMS AS:

TITLE OF INVENTION: RHEUMATOID ARTHRITIS, ME

FILE REFERENCE: CL001455

CURRENT APPLICATION NUMBER: US/60/455,444

CURRENT FILING DATE: 2003-03-18

NUMBER OF SEQ ID NOS: 50986

SOFTMARE: FASTER FOR Windows Version 4.0

SEQ ID NO 8193

LENGTH: 424
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1: /cgn2_6/ptodata/1/pubpaa/PUS_PUBCOMB.pep:*

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US-10-047-253-5
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US-10-340-578-68
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quence 8303,	equence 3492, P	equence 104, Ap	equence 2308	equence 3, 1	equence 474'	equence 84	equence 89,	quence 315	equence 529	equence 83,	equence 216	equence 157, Ap	equence 9,	equence 22	e 225,	equence 224,	equence 204	equence 27, Ap	equence 4756, A	equence 4547	equence 2652	equence 25,	equence 2273	equence 78,	equence 26, App	equence 2308	Sequence 166644,	equence 4332

# ALIGNMENTS

RESULT 1 US-10-046-961-7

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Sequence 7, Application US/10046961

Publication NO. US20020156012A1

GENERAL INFORMATION;
APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY
APPLICANT: LYAPINA, Svetlana
APPLICANT: VERMA, Rati
APPLICANT: DESHAIRS, Raymond
TITLE OF INVENTION: REGULATION OF TARGET PROTEIN ACTIVITY THROUGH MODIFIER PROTEINS
FILE REFERENCE: CIT1510-3

CURRENT APPLICATION NUMBER: US/10/046,961
CURRENT APPLICATION NUMBER: US 60/261,314
PRIOR APPLICATION NUMBER: US 60/261,314
PRIOR APPLICATION NUMBER: US 60/322,322
PRIOR APPLICATION NUMBER: US 60/322,322
PRIOR FILING DATE: 2001-09-14
PRIOR PRIOR PRIOR PROTEIN ACTIVITY THROUGH MODIFIER PROTEINS
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Best Local S
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CURRENT FILING DATE: 2003-01-09
PRIOR APPLICATION NUMBER: US 60/355,334
PRIOR FILING DATE: 2002-02-06
PRIOR PPLICATION NUMBER: US 10/047,253
PRIOR PPLICATION NUMBER: US 10/046,961
PRIOR PPLICATION NUMBER: US 10/046,961
PRIOR PILING DATE: 2002-01-14
PRIOR PILING DATE: 2002-01-14
PRIOR PILING DATE: 2002-01-14
PRIOR PILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: US 60/22,322
PRIOR APPLICATION NUMBER: US 60/322,322
PRIOR PILING DATE: 2001-01-12
PRIOR PILING DATE: 2001-01-12
PRIOR PILING DATE: 2001-01-12
PRIOR PILING DATE: 2001-09-14
PRIOR PILING DATE: 2001-09-14
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Best Local S
Matches 424
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Publication No. US20030153097A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY APPLICANT: DESHAIES, Raymond J. APPLICANT: COPE, Gregory
                                                                                                                                                                                                                                                              -10-340-578-66
                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/322,030 PRIOR FILING DATE: 2001-09-14 NUMBER OF SEQ ID NOS: 83
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TITLE OF INVENTION: MODULATION OF COP9 SIGNALSOME ISOPEPTIDASE ACTIVITY
FILE REFERENCE: CIT1590-1
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TYPE: PF
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; TYPE: PRT
; ORGANISM: Homo s
US-10-047-253-7
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Publication No. US20030166243A1
GENERAL INFORMATION:
APPLICANT: CALIFORNIA INSTITUTE OF TI
APPLICANT: COPE, Gregory
APPLICANT: VERMA, Rati
APPLICANT: VERMA, Rati
APPLICANT: KOONIN, Eugene
APPLICANT: KOONIN, Eugene
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APPLICANT: ARAVIND, L.
APPLICANT: COONIN, Eugene
APPLICANT: DESHALES, Raymond
APPLICANT: DESHALES, Raymond
TITLE OF INVENTION: REGULATION OF TARGET PROTEIN ACTIVITY THROUGH MODIFIER PROTEINS
FILE REFERENCE: CIT1510-4
CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: US 60/261,314
PRIOR APPLICATION NUMBER: US 60/261,314
PRIOR FILING DATE: 2001-09-14
PRIOR FILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: US 60/322,322
PRIOR APPLICATION NUMBER: US 60/322,322
PRIOR APPLICATION NUMBER: US 60/322,323
PRIOR APPLICATION NUMBER: US 60/322,030
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 22
SOFFWARE: Patentin version 3.1
SEQ ID NO 7
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Best Local Similarity
Matches 424; Conserv
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Pred. No. 3e-174;
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GENERAL INFORMATION:

APPLICANT: SUGAMURA, KAZUO

APPLICANT: TANAKA, Nobuyuki

TITLE OF INVENTION: Protein AMSH and cDNA thereof

FILE REFERENCE: 2003-0182/MMC/00653

CURRENT APPLICATION NUMBER: US/10/671,572A

CURRENT FILING DATE: 2003-09-29

PRIOR APPLICATION NUMBER: 09/831,452

PRIOR FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: PCT/JP99/06309

PRIOR APPLICATION NUMBER: DI/JP99/06309

PRIOR FILING DATE: 1999-11-12

PRIOR APPLICATION NUMBER: JP NO. 10-322674

PRIOR FILING DATE: 1998-11-12

PRIOR TILING DATE: 1998-11-12

PRIOR APPLICATION NUMBER: DI/JP99/06309

PRIOR FILING DATE: 1998-11-12

PRIOR FILING DATE: 1998-11-12
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US-10-671-572A-1
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US-10-671-572A-1
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LENGTH: 424
TYPE: PRT
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Best Local S
Matches 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 100.0%; Score 2208; DB 16; Length 424; Local Similarity 100.0%; Pred. No. 3e-174;
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                                                           IPKQSAGSDYCNTENEEELFLIQDQQGLITLGWIHTHPTQTAFLSSVDLHTHCSYQMMLP
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RESULT 6
US-10-046-961-5
; Sequence 5, Application US/10046961
; Publication No. US20020156012A1
; GENERAL INFORMATION:
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US-10-671-572A-3
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Best Local S
Matches 354
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TYPE: PRT
ORGANISM: mouse
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Sequence 3, Application US/10671572A

BUBLICANT: SUGAMURA, Kazuo
APPLICANT: SUGAMURA, Kazuo
APPLICANT: TANAKA, Nobuyuki
ITILE OF INVENTION: Protein AMSH and cDNA thereof
FILE REFERENCE: 2003-1382/WMC/00653

CURRENT APPLICATION NUMBER: US/10/671,572A

CURRENT FILING DATE: 2003-09-29
PRIOR APPLICATION NUMBER: 09/831,452
PRIOR APPLICATION NUMBER: DCT/JP99/06309
PRIOR APPLICATION NUMBER: DCT/JP99/06309
PRIOR APPLICATION NUMBER: JP NO. 10-322674
PRIOR PRIVING DATE: 1998-11-12
PRIOR APPLICATION NUMBER: JP NO. 10-322674
PRIOR PRIVING DATE: 1908-11-12
PRIOR APPLICATION NUMBER: JP NO. 10-322674
PRIOR PRIVING DATE: 1908-11-12
PRIOR APPLICATION NUMBER: JP NO. 10-322674
PRIOR PRIVING DATE: 1908-11-12
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ESIAIVCSPKFQETGFFKLTDYGLQEISTCRQKGFHPHGRDPPLFCDCSHVTVKDRIVTI
                                                        ESVAIVCSPKFQETGFFKLTDHGLEEISSCRQKGFHPHSKDPPLFCSCSHVTVVDRAVTI
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RESULT 7
US-10-340-578-67
; Sequence 67, Application US/10340578
; Publication No. US20030153097A1
; GENERAL INFORMATION:
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LENGTH: 421
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Best Local
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APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY
APPLICANT: DESHAIES, Raymond J.
APPLICANT: COPE, Gregory
APPLICANT: VERMA, Rati
APPLICANT: VERMA, Rati
APPLICANT: AMBROGGIO, Xavier I.
TITLE OF INVENTION: MODULATION OF COP9 SIGNALSOME ISOPEPTIDASE
FILE REFERENCE: CIT1590-1
CURRENT APPLICATION NUMBER: US/10/340,578
CURRENT FILING DATE: 2003-01-09
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ORGANISM: Homo
-10-046-961-5
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TITLE OF INVENTION: REGULATION OF TARGET PROTEIN ACTIVITY THROUGH MODIFIER PROTEINS
FILE REFERENCE: CIT1510-3
CURRENT APPLICATION NUMBER: US/10/046,961
CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: US 60/261,314
PRIOR FILING DATE: 2001-01-12
PRIOR FILING DATE: 2001-09-14
PRIOR PRIOR PRIOR DATE: 2001-09-14
PRIOR FILING DATE: 2001-09-14
PRIOR PRIOR APPLICATION NUMBER: US 60/322,030
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.1
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                                                                                                                                             Sequence 5, Application US/10047253
publication No. US20030166243A1
GENERAL INFORMATION:
APPLICANT: CALIFICANIA INSTITUTE OF
APPLICANT: COPE, Gregory
APPLICANT: VERMA, Rati
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Best Local
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ORGANISM: Homo
-10-340-578-67
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PRIOR APPLICATION NUMBER: US 60/322,322
PRIOR FILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: US 60/322,030
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 83
APPLICANT: ARAVIND, L
APPLICANT: KOONIN, Eugene
APPLICANT: KOONIN, Eugene
APPLICANT: DESHAIES, Raymond
TITLE OF INVENTION: REGULATION OF TARGET |
FILE REFERENCE: CITISIO-4
CURRENT APPLICATION NUMBER: US/10/047,253
CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: US 60/261,314
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PRIOR FILING DATE: 2002-02-06
PRIOR APPLICATION NUMBER: US 10/047,253
PRIOR FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: US 10/046,961
PRIOR FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: US 60/261,314
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PRIOR FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: US 60/322,322
PRIOR APPLICATION NUMBER: US 60/322,030
PRIOR APPLICATION NUMBER: US 60/322,030
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PATENTIN VETSION 3.1
SEQ ID NO 5.
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-047-253-5
                                PRIOR APPLICATION NUMBER: US 60/261,314
PRIOR FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: US 60/322,322
PRIOR FILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: US 60/322,030
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.1
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Best Local S
Matches 240
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                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/10046961 Publication No. US20020156012A1
                                                                                                                                                                            APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY
APPLICANT: LYAPINA, Svetlana
APPLICANT: VERMA, Rati
APPLICANT: DESHAIES, Raymond
TITLE OF INVENTION: REGULATION OF TARGET PROTEIN ACTIVITY THROUGH MODIFIER PROTEINS
FILE REFERENCE: CIT1510-3
CURRENT APPLICATION NUMBER: US/10/046,961
CURRENT FILING DATE: 2002-01-14
                     ID NO 6
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Best Local Similarity
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US-10-046-961-6
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                        YQMMLPESVAIVCSPKFQETGFFKLTDHGLEEISSCRQKGFHPHSKDPPLF 405
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56.4%; Pred. No. 4e-93;
ative 72; Mismatches
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US-10-340-578-68

RESULT 10

US-10-340-578-68

Sequence 68, Application US/10340578

Publication No. US20030153097A1

GENERAL INFORMATION:
APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY

APPLICANT: CDESHAIES, Raymond J.
APPLICANT: COPE, Gregory

APPLICANT: COPE, Gregory

APPLICANT: AMBROGGIO, Xavier I.
TITLE OF INVENTION: MODULATION OF COPP SIGNALSOME ISOPEPTIDASE ACTIVITY

FILE REBERENCE: CIT1590-1

CURRENT APPLICATION NUMBER: US 60/355,334

PRIOR TILING DATE: 2002-01-09

PRIOR APPLICATION NUMBER: US 10/047,253

PRIOR APPLICATION NUMBER: US 10/046,961

PRIOR APPLICATION NUMBER: US 10/046,961

PRIOR APPLICATION NUMBER: US 60/261,314

PRIOR PILING DATE: 2002-01-14

PRIOR APPLICATION NUMBER: US 60/22,322

PRIOR APPLICATION NUMBER: US 60/261,314

PRIOR APPLICATION NUMBER: US 60/322,322

PRIOR APPLICATION NUMBER: US 60/322,322

PRIOR PRIOR PRIING DATE: 2001-09-14

PRIOR PRIING DATE: 2001-09-14

PRIOR PRIING DATE: 2001-09-14

PRIOR FILING DATE: 2001-09-14

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PRIOR DATE: PRIOR DATE
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55.7%; 56.4%;

Score 1229.5; DB 14; Pred. No. 4e-93;

Length 461;

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RESULT 11
US-10-047-253-6
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Publication No. US20030166243A1
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LENGTH: 4
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Best Local
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-10-047-253-6
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                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/047,253
CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: US 60/261,314
PRIOR FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: US 60/322,322
PRIOR APPLICATION NUMBER: US 60/322,322
PRIOR APPLICATION NUMBER: US 60/322,030
PRIOR APPLICATION NUMBER: US 60/322,030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: ARAVIND, L
APPLICANT: KOONIN, Eugene
APPLICANT: DESHAIES, Raymond
TITLE OF INVENTION: REGULATION OF TARGET PROTEIN ACTIVITY THROUGH MODIFIER PROTEINS
FILE REFERENCE: CIT1510-4
                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.1
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Pred. No. 4e-93;
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US-10-012-600B-167
US-10-012-600B-167, Application US/10012600B
; Publication No. US20030064377A1
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APPLICANT: Recipon, Herve
APPLICANT: Chen, Sei-Yu
TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific Genes and I
TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific Genes and I
TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific Genes and I
TITLE OF INVENTION: COMPOSITION OF SECURE OF SUCH APPLICATION NUMBER: US/10/012,600B
CURRENT FILING DATE: 2001-11-06
PRIOR APPLICATION NUMBER: US 60/246,109
PRIOR FILING DATE: 2000-11-06
NUMBER OF SEQ ID NOS: 240
SOPTWARE: Patentin version 3.1
SEQ ID NO 167
SPOID NO 167
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Matches
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TYPE: PRT
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                                                                                                                                                                                  RSLKPGALSNSESIPTIDGLRHVVVPGRLCPQFLQLASANTARGVETCGILCGKLMRNEF
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                                                                                                                                                                                                                                                                                                                                    YNEEKKKEAEELARNMAIQQELEKEKQRVAQQKQQQLEQEQFHAFEEMIRNQELEKERLK 180
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                                     AOWNTESAVIACSEKEGELEEKTLDHGTEEISSCKOKGEHEHSKODEFE
                                                                          TITHVIVEXQSAGEDYCOMENVEELFNVQDQHDLLTLGWIHTHETQTAFLSSVDLHTHCS
                                                                                                             TITHYLIPKOSAGSDYCNTENEEELFLIQDQQGLITLGWIHTHPTQTAFLSSVDLHTHCS
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Pred. No. 4e-93;
72; Mismatches
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Sequence 2064, Application US/10104047
Publication No. US20030236392A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. US20030236392A1e1 fu
FILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:
PRIOR SEQ ID NOS: 4096
SOFTWARE: PATHON COMMANDER:
PRIOR OF SEQ ID NOS: 4096
SOFTWARE: PATHON COMMANDER:
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SOFTWARE: PATHON COMMANDER: 4096
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SOFTWARE: 4
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US-10-424-599-230882
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US-10-104-047-2064
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Publication No. US20040031072A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 230882
LENGTH: 519
TYPE: PRT
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Best Local
   Best Local Similarity 29.7
Matches 154; Conservative
                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(5323)B CURRENT APPLICATION NUMBER: US/10/424,599 CURRENT FILING DATE: 203-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: La Rosa Thomas
APPLICANT: Kovalic David
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
                                                                                                                                                                                  ORGANISM: Glycine max FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 35.1%; Score 774.5; DB 15; Length Local Similarity 53.6%; Pred. No. 9.3e-56; ndels 149; Conservative 45; Mismatches 69; Indels
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: Zhou Yihua
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25.2%; Score 557.5; DB 12; Length 29.7%; Pred. No. 2.3e-37; tive 82; Mismatches 171; Indels
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                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Soy Nucleic Acid Molec
TITLE OF INVENTION: Plants and Uses There
FILE REFERENCE: 38-21(5223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 166616
LENGTH: 504
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Publication No. US20040031072A1
GENERAL INFORMATION:
                                                                                                                                                                            Matches
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Best Local
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APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
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                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Clone ID: PAT_MRT3847_12146C.1.pep
                                                                                                                                                                                                                                                                                                                            ORGANISM: Glycine
                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
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                                                                                                                             LSQLGSAVEVNEDIPPRRYFRSGVEIIRMASIYSEEGNIEHAFILYNKYITLFIEKLPKH
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                                       RDYKSAVIPEKKDTVKKLKEIAFPKAEELKAELLKRYTKEYTEYNEEKKKE--AEELARN
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Search completed: August 17, 2004, 15:04:41 Job time : 48 secs

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1: /cgm2_6/ptodata/2
2: /cgm2_6/ptodata/2
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/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
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US-09-688-188B-89
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US-09-418-710-70
US-09-648-188B-14
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US-09-645-456A-13
US-09-645-991-13
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                                              sequence 89, Appl
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US-09-645-791-34	5-324A-	-456A-	US-09-579-664B-14	US-09-393-569-2	US-09-645-791-11	-425-324A-1	US-09-645-456A-11	US-09-740-235-1	US-09-976-594-507	US-09-543-681A-6274	US-09-418-710-21	US-09-718-815-2	US-09-718-852-2	US-09-718-692-2	US-09-266-225D-10	US-09-637-145-4	5180810-1
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## ALIGNMENTS

Minimum Maximum

Database

Title: Perfect

Run

on:

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APPLICANT: Itch, Funiko
APPLICANT: Itch, Susumu
APPLICANT: Heldin, Carl-Henrik
APPLICANT: Hendin, Carl-Henrik
APPLICANTON SMAD ASSOCIATING POLYPEPTIDES
FILE REFERENCE: L00461.70096.US
CURRENT APPLICATION NUMBER: US/09/665,479A
CURRENT FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US 60/154,846
PRIOR FILING DATE: 1999-09-20
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.2
SEQ ID NO 2
LENGTH: 424
TYPE: PRT
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US-09-665-479A-2
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IPKQSAGSDYCNTENEEELFLIQDQQGLITLGWIHTHPTQTAFLSSVDLHTHCSYQMWLP 360
                                      IPKQSAGSDYCNTENEEELFLIQDQQGLITLGWIHTHPTQTAFLSSVDLHTHCSYQMMLP 360
                                                                                                                  ALSNSESIPTIDGLRHVVVPGRLCPQFLQLASANTARGVETCGILCGKLMRNEFTITHVL
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                                                                                                    APPLICANT: MARTINEZ, RICARDO
APPLICANT: WHYTE, DAVID
TITLE OF INVENTION: STEZO-RELATED PROTEIN KINASES
FILE REFERENCE: 038602/0328
CURRENT APPLICATION NUMBER: US/09/688,188B
CURRENT FILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: 09/291.417
PRIOR APPLICATION NUMBER: 09/291.417
PRIOR APPLICATION NUMBER: 09/291.417
PRIOR FILING DATE: 1998-04-14
PRIOR FILING DATE: 1998-04-14
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NUMBER OF SEQ ID NOS: 155
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CURRENT APPLICATION DATA:
APPLICATION UMBER: US/07/409,658
FILING DATE: 18-SEP-1989
;SEQ ID NO: 2:
;SEQ ID NO: 2:
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                                                                                                                                                                                                                                                                      Sequence 89, Application US/09688188B Patent No. 6656716
GENERAL INFORMATION:
APPLICANT: PLOWMAN, GREGORY
APPLICANT: MARTINEZ, RICARDO
APPLICANT: WHYTE, DAVID
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                                                                       SEQ ID NO 89
                                                                                      SOFTWARE:
               TYPE: PRT
ORGANISM: Murine
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21.2%;
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Pred. No. 0.0067;
6; Mismatches 10
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US-09-291-417D-89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 50
                                                               Sequence 13, Application US/096881888 Patent No. 6656716 GENERAL INFORMATION:
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APPLICANT: PLOWMAN, GREGORY
APPLICANT: MARTINEZ, RICARDO
APPLICANT: MHYTE, DAVID
TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
FILE REFERENCE: 038602/0329
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 89
              APPLICANT: PLOWMAN, GREGORY APPLICANT: MARTINEZ, RICARI APPLICANT: WHYTE, DAVID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/081,784
PRIOR FILING DATE: 1998-04-14
NUMBER OF SEQ ID NOS: 155
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/291,417D CURRENT FILING DATE: 1999-04-13
TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1233
TYPE: PRT
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ORGANISM: Murine
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Local Similarity 21.9%;
les 50; Conservation
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                                                                                                                                                                                                                                                                                               138 IQQE---LEKEKORVAQQKQ---QQLEQEQFHAFEEMIRNQELEKERLKIVQBFGKVDPG 191
                                                                                                                                                                                                                                                                                                                                                                                                           327
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                                                                                                                                                                                                                                                                                                                                   YKROLLABROKRIEQOKEORRRIEEOORRERBARROOEREORRREQBEKRRIEELERRRK 445
                                                                                                                                                                                                                                                                                                                                                                  YKSAVIPEKKDTVKKLKE--IAFPKAEELKAELLKRYTKEYTEYNEEKKKEAEELARNMA 137
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                                                                                                                                                                                                                                                                 EEEERRRAEEEKRRVEREQEYIRRQLEEEQRHL--EILQQQLLQEQAM
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Pred. No. 0.023;
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Pred. No. 0.023;
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Sequence 13, Application US/09291417D
Patent NO. 6680170
GENERAL INFORMATION:
APPLICANT: PLOWMAN, GREGORY
APPLICANT: MARTINEZ, RICARDO
APPLICANT: MARTINEZ, RICARDO
TITLE OF INVENTION. STE20-RELATED PROTEIN KINASES
FILE REFERENCE: 038602/0329
CURRENT APPLICATION NUMBER: US/09/291,417D
CURRENT FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: 60/081,784
PRIOR FILING DATE: 1998-04-14
NUMBER OF SEQ ID NOS: 155
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 13
LENGTH: 1239
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CURRENT APPLICATION NUMBER: US/09/688,188B
CURRENT FILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: 09/291,417
PRIOR FILING DATE: 1999-04-14
PRIOR APPLICATION NUMBER: 60/081,784
PRIOR FILING DATE: 1998-04-14
PRIOR FILING DATE: 1998-04-14
VUMBER OF SEO ID NOS: 155
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 13
LENGTH: 1239
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US-09-291-417D-13
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                                                                                                Query Match
                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                  Local
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                                                                                Similarity
EEEEEVPEQEGEPSSIVNVPGESTLRRDFLRLQQENKERSEALRRQQL-LQEQQLREQEE
                              EVNEDIPPRRYFRS-----GVEIIRMASIYSEEGNIEHAFILYNKYITLFIEKLPKHRD
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                                                              5.4%; Score 119; DB 4; ilarity 21.2%; Pred. No. 0.081; Conservative 57; Mismatches 108
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                                                                  108;
                                                                                              Length 1239;
                                                                  Indels
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CURRENT APPLICATION NUMBER: US/09/418,710
CURRENT FILING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: PCT/JP98/01783
PRIOR FILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: JP 9/310027
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: JP 9/116570
PRIOR FILING DATE: 1997-04-18
NUMBER: OF SEQ ID NOS: 73
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 70
LENGTH: 1673
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 70, Application US/09418710
Patent No. 6596482
; GENERAL INFORMATION:
APPLICANT: Jones, Michael H.
TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
FILE REFERENCE: 06501-042001
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US-09-418-710-70
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KELLEKLOSAIACTNIFPLGRDRMYRRYWIFPSLPGLFIEEDYSGLTEDHLLPRPSSFQN
                                             PGLGG----
                                                                                          MFTEDEDDPGSHKRGRRGKRGQNGFKEFTRQEQINCVTRELLTADEEEALK--QEHQRKE
                                                                                                                                    QF-----EKERLKIVQEFGKVD 189
                                                                                                                                                                                       KRKEEKLKEQEQKWKEKQEKLKEDEQRNSTADISIGEEEREDFDTSIESKDTEQKELDQD
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TVRPAKPPVVDRSLKPGALSNSESIPTID-GLRH------VVVPGR-----LCPQFLQ 269

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US-09-291-417D-14
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US-09-688-188B-14
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APPLICANT: PLOWMAN, GREGORY
APPLICANT: MATTINEZ, RICARI
APPLICANT: WHYTE, DAVID
                                                                               GENERAL INFORMATION:
APPLICANT: PLOWMAN, GREGORY
APPLICANT: MARTINEZ, RICARDO
APPLICANT: WHYTE, DAVID
TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
FILE REFERENCE: 038602/0329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
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                                                                                                                                                                                                       Sequence 14, Application US/09291417D Patent No. 6680170
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Best Local
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CURRENT FILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: 09/291,417
PRIOR FILING DATE: 1999-04-14
PRIOR APPLICATION NUMBER: 60/081,784
PRIOR PILING DATE: 1998-04-14
PRIOR FILING DATE: 1998-04-14
NUMBER OF SEQ ID NOS: 155
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APPLICANT: WHYTE; DAVID
TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
FILE REFERENCE: 038602/0328
CURRENT APPLICATION NUMBER: US/09/291,417D CURRENT FILING DATE: 1999-04-13 PRIOR APPLICATION NUMBER: 60/081,784 PRIOR FILING DATE: 1998-04-14
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: F1, C. Alan
TITLE OF INVENTION: NOVEL GERMINAL CENTER KINASE CELL CYCLE PROTEINS, COMPOSITIONS ANI
TITLE OF INVENTION: METHODS OF USE
TITLE OF INVENTION: METHODS OF USE
TILE REFERENCE: A-68344/RMS/DHR
CURRENT FILLING DATE: 2000-08-24
CURRENT FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US/09/425,324
PRIOR APPLICATION NUMBER: US/09/425,324
PRIOR FILING DATE: 1999-10-21
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin version 3.1
SEQ ID NO 13
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SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 14
LENGTH: 1297
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Best Local S
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ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1324
                                                                                                                                                                                                                                                                                                                              y Match 5.3%;
Local Similarity 23.7%;
hes 50; Conservative 5
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PVDPQIPHLVAVKSQGP-ALTASQSVHEQPT 587
                                                                                  PSEKPAWAKEVEERSRLNROSSPAMPHKVANRISDPNLPPRSESFSISGVOPARTPPMLR
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                                       PAKPP----VVDRSLKPGALSNSESI---PT 250
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Pred. No. 0.11;
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                                                                                                                                    ; OTHER INFORMATION: synthetic US-09-645-791-13
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Patent No. 6562591
GENERAL INFORMATION:
APPLICANT: Fu, C. Alan
TITLE OF INVENTION: NOVEL GERMINAL CENTER KINASE CELL CYCLE PROTEINS, COMPOSITIONS
TITLE OF INVENTION: METHODS OF USE
FILE REFERENCE: A-68344/RMS/DHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 13, Approx No. 6569658
                                                               Matches
                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/645,791
CURRENT FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 09/425,324
PRIOR FILING DATE: 1999-10-21
NUMBER OF SEQ ID NOS: 36
                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Luo, Ying
APPLICANT: Fu, Alan C
APPLICANT: Shen, Mary
TITLE OF INVENTION: NOVEL GERMINAL CENTER KINASE CELL CYCLE PROTEINS; COMPOSITIONS
TITLE OF INVENTION: METHODS OF USE
FILE REFERENCE: A-68344-1/RMS/DHR
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CURRENT FILING DATE: 1999-10-21
CURDEN OF SEQ ID NOS: 36
SOFTWARE: Patentin version 3.1
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TYPE: PRT
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ORGANISM: Artificial sequence
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KHRDYKSAVIPEKKOTVKKLKE--IAFPKAEELKAELLKRYTKEYTEYNEEKKKEAEELA 133
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                                                         Score 118; DB 4;
Pred: No. 0.11;
0; Mismatches 73
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US-09-425-324A-9
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US-09-645-456A-9
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Patent No. 6562580
SOFTWARE: SEQ ID NO 9
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Best Local
                              APPLICANT: Fu, C. Alan
TITLE OF INVENTION: NOVEL GERMINAL CENTER I
TITLE OF INVENTION: METHODS OF USE
FILE REFERENCE: A-68344/RMS/DHR
CURRENT APPLICATION NUMBER: US/99/425,324A
CURRENT FILING DATE: 1999-10-21
NUMBER OF SEQ ID NOS: 36
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PRIOR FILING DATE: 1999-10-21
NUMBER OF SEQ ID NOS: 36
SOFTWARE: """
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TITLE OF INVENTION: NOVEL GERMINAL CENTER KINASE CELL CYCLE
TITLE OF INVENTION: METHODS OF USE
FILE REFERENCE: A-68344/RMS/DHR
CURRENT APPLICATION NUMBER: US/09/645,456A
CURRENT FILING DATE: 2000-08-24
CURRENT FILING DATE: 12000-08-24
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; OTHER INFORMATION: synthetic
US-09-645-791-9
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US-09-645-791-9
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APPLICANT: LUC, YING
APPLICANT: FU, Alan C
APPLICANT: Shen, MATY
TITLE OF INVENTION: MOVEL GERMINAL CENTER KINASE CELL CYCLE PROTEINS; COMPOSITIONS /
TITLE OF INVENTION: METHODS OF USE
TILE REFERENCE: A-68344-1/RMS/DHR
CURRENT APPLICATION NUMBER: US/09/645,791
CURRENT APPLICATION NUMBER: US/09/645,791
CURRENT FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 09/425,324
PRIOR APPLICATION NUMBER: US 09/425,324
PRIOR FILING DATE: 1999-10-21
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.1
SEQ ID NO
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Best Local Similarity
Matches 50; Conserv
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TYPE: PRT
ORGANISM: Artificial sequence
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                                                                                                                                                                                                                                                                                         76 KHRDYKSAVIPEKKOTVKKLKE--IAFPKABELKABLLKRYTKEYTEYNEEKKKEABBLA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAKPP----VVDRSLKPGALSNSESI----PT 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PSEKPAWAKEVEERSRINROSSPAMPHKVANRISDPNIPPRSESFSISGVOPARTPPMIR 557
      PVDPQIPHLVAVKSQGP-ALTASQSVHEQPT 587
                                                                                                                                                                     RABHEQEYKRKQLEEQRQAERLQRQLKQERDYLVSLQHQRQBQRPVBKKPLYHYKBGMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/09645791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------KIVQEFGKVD----PGLGGPLVPDLEKPSLDV-FPTLTVSSIQPSDCHTTVR 226
                                             PAKPP----VVDRSLKPGALSNSESI---PT 250
                                                                                       PSEKPAWAKEVEERSRLNROSSPAMPHKVANRISDPNLPPRSESFSISGVOPARTPPMLR
                                                                                                                          -----KIVQEFGKVD----PGLGGPLVPDLEKPSLDV-FPTLTVSSIQPSDCHTTVR
                                                                                                                                                                                                                                                                                                                                5.3%; Score 118; DB 4; Length 1332; ilarity 23.7%; Pred. No. 0.11; Conservative 50; Mismatches 73; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73; Indels 38;
                                                                                                                                                                                                                                                                                                                                       38;
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                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                       497
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                                                                                       557
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                                                                                                                                                                                                               179
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